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Wed Aug 28 08:39:01 2001 [BLASTN 2.1.3 [Apr-1-2001], NCBI]

Repeats masked (summary below)

/home/ruby/va/Molbio/carpenda/tempids/ss.DNA44804 (2555 bp) TECH CENTER 1600/2900

Sequences producing High-scoring Segment Pairs:	Frame	Score	Match	Pct	E-val
1 P_AAA49564 Human PRO357 cDNA.	+	2555	2555	100	0.0
2 P_AAA46922 cDNA encoding novel polypeptide PRO357.	+	2555	2555	100	0.0
3 P_AAX80056 Human PRO357 nucleotide sequence.	+	2555	2555	100	0.0
4 P_AAX87261 cDNA clone encoding human PRO357, amplif	+	2555	2555	100	0.0
5 P_AAA58765 cDNA encoding a leucine-rich surface gly	+	2142	2142	100	0.0
6 AC012676 Homo sapiens chromosome 16 clone RP11-29	+	2138	2141	100	0.0
7 AC005222 Homo sapiens chromosome 16, cosmid clone	+	2138	2141	100	0.0
8 P_AAF44105 Human PRO1282 (UNQ652) nucleotide sequen	+	2127	2139	100	0.0
9 P_AAF92065 Human PRO1282 cDNA.	+	2127	2139	100	0.0
10 P_AA264959 Membrane-bound protein PRO1282 encoding	+	2127	2139	100	0.0
11 AX092284 Sequence 15 from Patent WO0116318.	+	2127	2139	100	0.0
12 P_AAC69514 Human secreted protein gene 3 clone HSYA	+	2065	2135	99	0.0

>1 P_AAA49564 Human PRO357 cDNA. (2555 bp) [1 seg]
Score = 2555 (5065 bits), Expect = 0.0
Identities = 2555/2555 (100%), at 1,1-2555,2555, Strand +/+

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DNA44804      1 GGGGCGGGTGGACGCGGACTCGAACGCGAGTTGCTTCGGGACCCAGGACCCCTCGGGCCC
*****
P_AAA49564    1 GGGGCGGGTGGACGCGGACTCGAACGCGAGTTGCTTCGGGACCCAGGACCCCTCGGGCCC

DNA44804     61 GACCCGCCAGGAAAGACTGAGGCCGCGGCCTGCCCGCCCGGCTCCCTGCGCCGCCGCCG
*****
P_AAA49564    61 GACCCGCCAGGAAAGACTGAGGCCGCGGCCTGCCCGCCCGGCTCCCTGCGCCGCCGCCG

DNA44804    121 CCTCCCGGGACAGAAGATGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACT
*****
P_AAA49564   121 CCTCCCGGGACAGAAGATGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACT

DNA44804    181 GGCCCTGGGGCCTGGGGTGCAGGGCTGCCCATCCGGCTGCCAGTGCAGCCAGCCACAGAC
*****
P_AAA49564   181 GGCCCTGGGGCCTGGGGTGCAGGGCTGCCCATCCGGCTGCCAGTGCAGCCAGCCACAGAC

DNA44804    241 AGTCTTCTGCACTGCCCGCCAGGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGT
*****
P_AAA49564   241 AGTCTTCTGCACTGCCCGCCAGGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGT

DNA44804    301 GGGGCTGTACGTCTTTGAGAACGGCATCACCATGCTCGACGCAAGCAGCTTTGCCGGCCT
*****
P_AAA49564   301 GGGGCTGTACGTCTTTGAGAACGGCATCACCATGCTCGACGCAAGCAGCTTTGCCGGCCT

DNA44804    361 GCCGGGCCTGCAGCTCCTGGACCTGTACAGAACAGATCGCCAGCCTGCGCCTGCCCGG
*****
P_AAA49564   361 GCCGGGCCTGCAGCTCCTGGACCTGTACAGAACAGATCGCCAGCCTGCGCCTGCCCGG

DNA44804    421 CCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCGGCATCCTGGA
*****
P_AAA49564   421 CCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCGGCATCCTGGA

DNA44804    481 CACTGCCAACGTGGAGGCGCTGCGGCTGGCTGGTCTGGGGCTGCAGCAGCTGGACGAGGG
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BLAST RESULTS A-1

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*****
P_AAA49564 481 CACTGCCAACGTGGAGGCGCTGCGGCTGGCTGGTCTGGGGCTGCAGCAGCTGGACGAGGG
DNA44804 541 GCTCTTCAGCCGCTTGCGCAACCTCCACGACCTGGATGTGTCCGACAACCAGCTGGAGCG
*****
P_AAA49564 541 GCTCTTCAGCCGCTTGCGCAACCTCCACGACCTGGATGTGTCCGACAACCAGCTGGAGCG
DNA44804 601 AGTGCCACCTGTGATCCGAGGCGCTCCGGGGCGCTGACGCGCCTGCGGCTGGCCGGCAACAC
*****
P_AAA49564 601 AGTGCCACCTGTGATCCGAGGCGCTCCGGGGCGCTGACGCGCCTGCGGCTGGCCGGCAACAC
DNA44804 661 CCGCATTGCCCAGCTGCGGCCCGAGGACCTGGCCGGCCTGGCTGCCCTGCAGGAGCTGGA
*****
P_AAA49564 661 CCGCATTGCCCAGCTGCGGCCCGAGGACCTGGCCGGCCTGGCTGCCCTGCAGGAGCTGGA
DNA44804 721 TGTGAGCAACCTAAGCCTGCAGGCCCTGCCTGGCGACCTCTCGGGCCTCTTCCCCGCCT
*****
P_AAA49564 721 TGTGAGCAACCTAAGCCTGCAGGCCCTGCCTGGCGACCTCTCGGGCCTCTTCCCCGCCT
DNA44804 781 GCGGCTGCTGGCAGCTGCCC GCAACCCCTTCAACTGCGTGTGCCCCCTGAGCTGGTTTGG
*****
P_AAA49564 781 GCGGCTGCTGGCAGCTGCCC GCAACCCCTTCAACTGCGTGTGCCCCCTGAGCTGGTTTGG
DNA44804 841 CCCCTGGGTGCGCGAGAGCCACGTACACTGGCCAGCCCTGAGGAGACGCGCTGCCACTT
*****
P_AAA49564 841 CCCCTGGGTGCGCGAGAGCCACGTACACTGGCCAGCCCTGAGGAGACGCGCTGCCACTT
DNA44804 901 CCCGCCAAGAACGCTGGCCGGCTGCTCCTGGAGCTTGA CTACGCCGACTTTGGCTGCCC
*****
P_AAA49564 901 CCCGCCAAGAACGCTGGCCGGCTGCTCCTGGAGCTTGA CTACGCCGACTTTGGCTGCCC
DNA44804 961 AGCCACCACCACCACAGCCACAGTGCCCACCACGAGGCCCGTGGTGCGGGAGCCACAGC
*****
P_AAA49564 961 AGCCACCACCACCACAGCCACAGTGCCCACCACGAGGCCCGTGGTGCGGGAGCCACAGC
DNA44804 1021 CTTGTCTTCTAGCTTG GCTCCTACCTGGCTTAGCCCCACAGCGCCGGCCACTGAGGCCCC
*****
P_AAA49564 1021 CTTGTCTTCTAGCTTG GCTCCTACCTGGCTTAGCCCCACAGCGCCGGCCACTGAGGCCCC
DNA44804 1081 CAGCCCGCCCTCCACTGCCCCACCGACTGTAGGGCCTGTCCCCCAGCCCCAGGACTGCCC
*****
P_AAA49564 1081 CAGCCCGCCCTCCACTGCCCCACCGACTGTAGGGCCTGTCCCCCAGCCCCAGGACTGCCC
DNA44804 1141 ACCGTCCACCTGCCTCAATGGGGGCACATGCCACCTGGGGACACGGCACCACCTGGCGTG
*****
P_AAA49564 1141 ACCGTCCACCTGCCTCAATGGGGGCACATGCCACCTGGGGACACGGCACCACCTGGCGTG
DNA44804 1201 CTTGTGCCCCGAAGGCTTACGGGCCTGTACTGTGAGAGCCAGATGGGGCAGGGGACACG
*****
P_AAA49564 1201 CTTGTGCCCCGAAGGCTTACGGGCCTGTACTGTGAGAGCCAGATGGGGCAGGGGACACG
DNA44804 1261 GCCCAGCCCTACACCAGTCACGCCGAGGCCACCACGGTCCCTGACCCTGGGCATCGAGCC
*****
P_AAA49564 1261 GCCCAGCCCTACACCAGTCACGCCGAGGCCACCACGGTCCCTGACCCTGGGCATCGAGCC
DNA44804 1321 GGTGAGCCCCACCTCCCTGCGCGTGGGGCTGCAGCGCTACCTCCAGGGGAGCTCCGTGCA
*****

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BLAST RESULTS A-2

P_AAA49564 1321 GGTGAGCCCCACCTCCCTGCGCTGGGGCTGCAGCGCTACCTCCAGGGGAGCTCCGTGCA
DNA44804 1381 GCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCGGGCCCTGATAAGCGGCTGGTGAC

P_AAA49564 1381 GCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCGGGCCCTGATAAGCGGCTGGTGAC
DNA44804 1441 GCTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTCACCCAGCTGCGGCCCAACGCCAC

P_AAA49564 1441 GCTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTCACCCAGCTGCGGCCCAACGCCAC
DNA44804 1501 TTACTCCGTCTGTGTTCATGCCTTTGGGGCCCGGGCGGGTGCCGGAGGGCGAGGAGGCCTG

P_AAA49564 1501 TTACTCCGTCTGTGTTCATGCCTTTGGGGCCCGGGCGGGTGCCGGAGGGCGAGGAGGCCTG
DNA44804 1561 CGGGGAGGCCCATACACCCCCAGCCGTCCACTCCAACCACGCCCCAGTCACCCAGGCCCG

P_AAA49564 1561 CGGGGAGGCCCATACACCCCCAGCCGTCCACTCCAACCACGCCCCAGTCACCCAGGCCCG
DNA44804 1621 CGAGGGCAACCTGCCGCTCCTCATTGCGCCCGCCCTGGCCGCGGTGCTCCTGGCCGCGCT

P_AAA49564 1621 CGAGGGCAACCTGCCGCTCCTCATTGCGCCCGCCCTGGCCGCGGTGCTCCTGGCCGCGCT
DNA44804 1681 GGCTGCGGTGGGGGCGAGCCTACTGTGTGCGGCGGGGCGGGCCATGGCAGCAGCGGCTCA

P_AAA49564 1681 GGCTGCGGTGGGGGCGAGCCTACTGTGTGCGGCGGGGCGGGCCATGGCAGCAGCGGCTCA
DNA44804 1741 GGACAAAGGGCAGGTGGGGCCAGGGGCTGGGCCCTGGAAGTGGAGGGAGTGAAGGTCCC

P_AAA49564 1741 GGACAAAGGGCAGGTGGGGCCAGGGGCTGGGCCCTGGAAGTGGAGGGAGTGAAGGTCCC
DNA44804 1801 CTTGGAGCCAGGCCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCAGCGGGTCTGA

P_AAA49564 1801 CTTGGAGCCAGGCCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCAGCGGGTCTGA
DNA44804 1861 GTGTGAGGTGCCACTCATGGGCTTCCCAGGGCCTGGCCTCCAGTCACCCCTCCACGCAA

P_AAA49564 1861 GTGTGAGGTGCCACTCATGGGCTTCCCAGGGCCTGGCCTCCAGTCACCCCTCCACGCAA
DNA44804 1921 GCCCTACATCTAAGCCAGAGAGAGACAGGGCAGCTGGGGCCGGGCTCTCAGCCAGTGAGA

P_AAA49564 1921 GCCCTACATCTAAGCCAGAGAGAGACAGGGCAGCTGGGGCCGGGCTCTCAGCCAGTGAGA
DNA44804 1981 TGGCCAGCCCCCTCCTGCTGCCACACCACGTAAGTTCTCAGTCCCAACCTCGGGGATGTG

P_AAA49564 1981 TGGCCAGCCCCCTCCTGCTGCCACACCACGTAAGTTCTCAGTCCCAACCTCGGGGATGTG
DNA44804 2041 TGCAGACAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGACCTCGGTCTCCTCA

P_AAA49564 2041 TGCAGACAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGACCTCGGTCTCCTCA
DNA44804 2101 TCTGTGAGATGCTGTGGCCCAGCTGACGAGCCCTAACGTCCCCAGAACCGAGTGCCTATG

P_AAA49564 2101 TCTGTGAGATGCTGTGGCCCAGCTGACGAGCCCTAACGTCCCCAGAACCGAGTGCCTATG
DNA44804 2161 AGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCACGGCGGGCCCTGCCA

P_AAA49564 2161 AGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCACGGCGGGCCCTGCCA

BLAST RESULTS A-3

DNA44804 2221 TGTGCTGGTAACGCATGCCTGGGCCCTGCTGGGCTCTCCCACTCCAGGCGGACCCTGGGG

 P_AAA49564 2221 TGTGCTGGTAACGCATGCCTGGGCCCTGCTGGGCTCTCCCACTCCAGGCGGACCCTGGGG
 DNA44804 2281 GCCAGTGAAGGAAGCTCCCGGAAAGAGCAGAGGGAGAGCGGGTAGGCGGCTGTGTGACTC

 P_AAA49564 2281 GCCAGTGAAGGAAGCTCCCGGAAAGAGCAGAGGGAGAGCGGGTAGGCGGCTGTGTGACTC
 DNA44804 2341 TAGTCTTGCCCCAGGAAGCGAAGGAACAAAAGAACTGGAAAGGAAGATGCTTTAGGAA

 P_AAA49564 2341 TAGTCTTGCCCCAGGAAGCGAAGGAACAAAAGAACTGGAAAGGAAGATGCTTTAGGAA
 DNA44804 2401 CATGTTTGTCTTTTTTAAAATATATATATATTTATAAGAGATCCTTTCCCATTTATTCTG

 P_AAA49564 2401 CATGTTTGTCTTTTTTAAAATATATATATATTTATAAGAGATCCTTTCCCATTTATTCTG
 DNA44804 2461 GGAAGATGTTTTTCAAACCTCAGAGACAAGGACTTTGGTTTTTGTAAAGACAAACGATGATA

 P_AAA49564 2461 GGAAGATGTTTTTCAAACCTCAGAGACAAGGACTTTGGTTTTTGTAAAGACAAACGATGATA
 DNA44804 2521 TGAAGGCCTTTTGTAAAGAAAAATAAAAAAAAAA

 P_AAA49564 2521 TGAAGGCCTTTTGTAAAGAAAAATAAAAAAAAAA

>2 P_AAA46922 cDNA encoding novel polypeptide PRO357. DNA, PAT 03-OCT-2000
 (2555 bp) [1 seg]
 Score = 2555 (5065 bits), Expect = 0.0
 Identities = 2555/2555 (100%), at 1,1-2555,2555, Strand +/+

DNA44804 1 GGGGCGGGTGGACGCGGACTCGAACGCGAGTTGCTTCGGGACCCAGGACCCCTCGGGCCC

 P_AAA46922 1 GGGGCGGGTGGACGCGGACTCGAACGCGAGTTGCTTCGGGACCCAGGACCCCTCGGGCCC
 DNA44804 61 GACCCGCCAGGAAAGACTGAGGCCGCGGCCTGCCCCGCCCGGCTCCCTGCGCCGCCGCCG

 P_AAA46922 61 GACCCGCCAGGAAAGACTGAGGCCGCGGCCTGCCCCGCCCGGCTCCCTGCGCCGCCGCCG
 DNA44804 121 CCTCCCGGACAGAAGATGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACT

 P_AAA46922 121 CCTCCCGGACAGAAGATGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACT
 DNA44804 181 GGCCCTGGGGCCTGGGGTGCAGGGCTGCCATCCGGCTGCCAGTGCAGCCAGCCACAGAC

 P_AAA46922 181 GGCCCTGGGGCCTGGGGTGCAGGGCTGCCATCCGGCTGCCAGTGCAGCCAGCCACAGAC
 DNA44804 241 AGTCTTCTGCACTGCCCCCAGGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGT

 P_AAA46922 241 AGTCTTCTGCACTGCCCCCAGGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGT
 DNA44804 301 GGGGCTGTACGTCTTTGAGAACGGCATCACCATGCTCGACGCAAGCAGCTTTGCCGGCCT

 P_AAA46922 301 GGGGCTGTACGTCTTTGAGAACGGCATCACCATGCTCGACGCAAGCAGCTTTGCCGGCCT
 DNA44804 361 GCCGGGCCTGCAGCTCCTGGACCTGTACAGAACAGATCGCCAGCCTGCGCCTGCCCGG

 P_AAA46922 361 GCCGGGCCTGCAGCTCCTGGACCTGTACAGAACAGATCGCCAGCCTGCGCCTGCCCGG

BLAST RESULTS A-A

DNA44804	421	CCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCGGCATCCTGGA

P_AAA46922	421	CCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCGGCATCCTGGA
DNA44804	481	CACTGCCAACGTGGAGGCGCTGCGGCTGGCTGGTCTGGGGCTGCAGCAGCTGGACGAGGG

P_AAA46922	481	CACTGCCAACGTGGAGGCGCTGCGGCTGGCTGGTCTGGGGCTGCAGCAGCTGGACGAGGG
DNA44804	541	GCTCTTCAGCCGCTTGCGCAACCTCCACGACCTGGATGTGTCCGACAACCAGCTGGAGCG

P_AAA46922	541	GCTCTTCAGCCGCTTGCGCAACCTCCACGACCTGGATGTGTCCGACAACCAGCTGGAGCG
DNA44804	601	AGTGCCACCTGTGATCCGAGGCGCTCCGGGGCTGACGCGCCTGCGGCTGGCCGGCAACAC

P_AAA46922	601	AGTGCCACCTGTGATCCGAGGCGCTCCGGGGCTGACGCGCCTGCGGCTGGCCGGCAACAC
DNA44804	661	CCGCATTGCCCAGCTGCGGCCCGAGGACCTGGCCGGCCTGGCTGCCCTGCAGGAGCTGGA

P_AAA46922	661	CCGCATTGCCCAGCTGCGGCCCGAGGACCTGGCCGGCCTGGCTGCCCTGCAGGAGCTGGA
DNA44804	721	TGTGAGCAACCTAAGCCTGCAGGCCCTGCCTGGCGACCTCTCGGGCCTCTTCCCCGCCT

P_AAA46922	721	TGTGAGCAACCTAAGCCTGCAGGCCCTGCCTGGCGACCTCTCGGGCCTCTTCCCCGCCT
DNA44804	781	GCGGCTGCTGGCAGCTGCCCCGAACCCCTTCAACTGCGTGTGCCCCCTGAGCTGGTTTGG

P_AAA46922	781	GCGGCTGCTGGCAGCTGCCCCGAACCCCTTCAACTGCGTGTGCCCCCTGAGCTGGTTTGG
DNA44804	841	CCCCTGGGTGCGCGAGAGCCACGTCACTGGCCAGCCCTGAGGAGACGCGCTGCCACTT

P_AAA46922	841	CCCCTGGGTGCGCGAGAGCCACGTCACTGGCCAGCCCTGAGGAGACGCGCTGCCACTT
DNA44804	901	CCCGCCCAAGAACGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCCGACTTTGGCTGCCC

P_AAA46922	901	CCCGCCCAAGAACGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCCGACTTTGGCTGCCC
DNA44804	961	AGCCACCACCACCACAGCCACAGTGGCCACCACGAGGCCCGTGGTGC GGAGCCACAGC

P_AAA46922	961	AGCCACCACCACCACAGCCACAGTGGCCACCACGAGGCCCGTGGTGC GGAGCCACAGC
DNA44804	1021	CTTGTCTTCTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCGGCCACTGAGGCCCC

P_AAA46922	1021	CTTGTCTTCTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCGGCCACTGAGGCCCC
DNA44804	1081	CAGCCCGCCCTCCACTGCCCCACCGACTGTAGGGCCTGTCCCCAGCCCCAGGACTGCCC

P_AAA46922	1081	CAGCCCGCCCTCCACTGCCCCACCGACTGTAGGGCCTGTCCCCAGCCCCAGGACTGCCC
DNA44804	1141	ACCGTCCACCTGCCTCAATGGGGGCACATGCCACCTGGGGACACGGCACCACTGGCGTG

P_AAA46922	1141	ACCGTCCACCTGCCTCAATGGGGGCACATGCCACCTGGGGACACGGCACCACTGGCGTG
DNA44804	1201	CTTGTGCCCCGAAGGCTTACGGGCTGTACTGTGAGAGCCAGATGGGGCAGGGGACACG

P_AAA46922	1201	CTTGTGCCCCGAAGGCTTACGGGCTGTACTGTGAGAGCCAGATGGGGCAGGGGACACG

BLAST RESULTS A-S

DNA44804	1261	CCCCAGCCCTACACCAGTCACGCCGAGGCCACCACGGTCCCTGACCCTGGGCATCGAGCC
P_AAA46922	1261	CCCCAGCCCTACACCAGTCACGCCGAGGCCACCACGGTCCCTGACCCTGGGCATCGAGCC
DNA44804	1321	GGTGAGCCCCACCTCCCTGCGCGTGGGGCTGCAGCGCTACCTCCAGGGGAGCTCCGTGCA
P_AAA46922	1321	GGTGAGCCCCACCTCCCTGCGCGTGGGGCTGCAGCGCTACCTCCAGGGGAGCTCCGTGCA
DNA44804	1381	GCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCGGGCCCTGATAAGCGGCTGGTGAC
P_AAA46922	1381	GCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCGGGCCCTGATAAGCGGCTGGTGAC
DNA44804	1441	GCTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTCACCCAGCTGCGGCCAACGCCAC
P_AAA46922	1441	GCTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTCACCCAGCTGCGGCCAACGCCAC
DNA44804	1501	TTACTCCGTCTGTGTCTATGCCTTTGGGGCCCGGGCGGGTGCCGGAGGGCGAGGAGGCCTG
P_AAA46922	1501	TTACTCCGTCTGTGTCTATGCCTTTGGGGCCCGGGCGGGTGCCGGAGGGCGAGGAGGCCTG
DNA44804	1561	CGGGGAGGGCCATACACCCCGAGCCGTCCACTCCAACCACGCCCCAGTCACCCAGGCCCCG
P_AAA46922	1561	CGGGGAGGGCCATACACCCCGAGCCGTCCACTCCAACCACGCCCCAGTCACCCAGGCCCCG
DNA44804	1621	CGAGGGCAACCTGCCGCTCCTCATTGCGCCCGCCCTGGCCGCGGTGCTCCTGGCCGCGCT
P_AAA46922	1621	CGAGGGCAACCTGCCGCTCCTCATTGCGCCCGCCCTGGCCGCGGTGCTCCTGGCCGCGCT
DNA44804	1681	GGCTGCGGTGGGGGAGCCTACTGTGTGCGGCGGGGCGGGCCATGGCAGCAGCGGCTCA
P_AAA46922	1681	GGCTGCGGTGGGGGAGCCTACTGTGTGCGGCGGGGCGGGCCATGGCAGCAGCGGCTCA
DNA44804	1741	GGACAAAGGGCAGGTGGGGCCAGGGGCTGGGCCCTGGAAGTGGAGGGAGTGAAGGTCCC
P_AAA46922	1741	GGACAAAGGGCAGGTGGGGCCAGGGGCTGGGCCCTGGAAGTGGAGGGAGTGAAGGTCCC
DNA44804	1801	CTTGAGCCAGGCCCCAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCAGCGGGTCTGA
P_AAA46922	1801	CTTGAGCCAGGCCCCAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCAGCGGGTCTGA
DNA44804	1861	GTGTGAGGTGCCACTCATGGGCTTCCCAGGGCCTGGCCTCCAGTCACCCCTCCACGCAA
P_AAA46922	1861	GTGTGAGGTGCCACTCATGGGCTTCCCAGGGCCTGGCCTCCAGTCACCCCTCCACGCAA
DNA44804	1921	GCCCTACATCTAAGCCAGAGAGAGACAGGGCAGCTGGGGCCGGGCTCTCAGCCAGTGAGA
P_AAA46922	1921	GCCCTACATCTAAGCCAGAGAGAGACAGGGCAGCTGGGGCCGGGCTCTCAGCCAGTGAGA
DNA44804	1981	TGGCCAGCCCCCTCTGCTGCCACACCACGTAAGTCTCAGTCCCAACCTCGGGGATGTG
P_AAA46922	1981	TGGCCAGCCCCCTCTGCTGCCACACCACGTAAGTCTCAGTCCCAACCTCGGGGATGTG
DNA44804	2041	TGCAGACAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGACCTCGGTCTCCTCA
P_AAA46922	2041	TGCAGACAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGACCTCGGTCTCCTCA
DNA44804	2101	TCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGAACCGAGTGCCTATG

BLAST RESULTS A-2

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*****
P_AAA46922 2101 TCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGAACCGAGTGCCTATG
DNA44804 2161 AGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCACGGCGGGCCCTGCCA
*****
P_AAA46922 2161 AGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCACGGCGGGCCCTGCCA
DNA44804 2221 TGTGCTGGTAACGCATGCCTGGGCCCTGCTGGGCTCTCCCACTCCAGGCGGACCCTGGGG
*****
P_AAA46922 2221 TGTGCTGGTAACGCATGCCTGGGCCCTGCTGGGCTCTCCCACTCCAGGCGGACCCTGGGG
DNA44804 2281 GCCAGTGAAGGAAGCTCCCGGAAAGAGCAGAGGGAGAGCGGGTAGGCGGCTGTGTGACTC
*****
P_AAA46922 2281 GCCAGTGAAGGAAGCTCCCGGAAAGAGCAGAGGGAGAGCGGGTAGGCGGCTGTGTGACTC
DNA44804 2341 TAGTCTTGGCCCCAGGAAGCGAAGGAACAAAAGAACTGGAAAGGAAGATGCTTTAGGAA
*****
P_AAA46922 2341 TAGTCTTGGCCCCAGGAAGCGAAGGAACAAAAGAACTGGAAAGGAAGATGCTTTAGGAA
DNA44804 2401 CATGTTTTGCTTTTTTAAATATATATATATTTATAAGAGATCCTTTCCCATTTATTCTG
*****
P_AAA46922 2401 CATGTTTTGCTTTTTTAAATATATATATATTTATAAGAGATCCTTTCCCATTTATTCTG
DNA44804 2461 GGAAGATGTTTTTCAAACCTCAGAGACAAGGACTTTGGTTTTTGTAGACAAACGATGATA
*****
P_AAA46922 2461 GGAAGATGTTTTTCAAACCTCAGAGACAAGGACTTTGGTTTTTGTAGACAAACGATGATA
DNA44804 2521 TGAAGGCCTTTTGTAGAAAAAATAAAAAAAAAA
*****
P_AAA46922 2521 TGAAGGCCTTTTGTAGAAAAAATAAAAAAAAAA

>3 P_AAX80056 Human PRO357 nucleotide sequence. (2555 bp) [1 seg]
Score = 2555 (5065 bits), Expect = 0.0
Identities = 2555/2555 (100%), at 1,1-2555,2555, Strand +/-

DNA44804 1 GGGGCGGTGGACGCGGACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCC
*****
P_AAX80056 1 GGGGCGGTGGACGCGGACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCC
DNA44804 61 GACCCGCCAGGAAAGACTGAGGCCGCGGCTGCCCCGCCCGGCTCCCTGCGCCGCCGCCG
*****
P_AAX80056 61 GACCCGCCAGGAAAGACTGAGGCCGCGGCTGCCCCGCCCGGCTCCCTGCGCCGCCGCCG
DNA44804 121 CCTCCCGGACAGAAGATGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACT
*****
P_AAX80056 121 CCTCCCGGACAGAAGATGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACT
DNA44804 181 GGCCCTGGGGCCTGGGGTGCAGGGCTGCCATCCGGCTGCCAGTGCAGCCAGCCACAGAC
*****
P_AAX80056 181 GGCCCTGGGGCCTGGGGTGCAGGGCTGCCATCCGGCTGCCAGTGCAGCCAGCCACAGAC
DNA44804 241 AGTCTTCTGCACTGCCCCCAGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGT
*****
P_AAX80056 241 AGTCTTCTGCACTGCCCCCAGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGT
DNA44804 301 GGGGCTGTACGTCTTTGAGAACGGCATCACCATGCTCGACGCAAGCAGCTTTGCCGGCCT
*****

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BLAST RESULTS A-7

P_AAX80056 301 GGGGCTGTACGTCTTTGAGAACGGCATCACCATGCTCGACGCAAGCAGCTTTGCCGGCCT

DNA44804 361 GCCGGGCCTGCAGCTCCTGGACCTGTCACAGAACCAGATCGCCAGCCTGCGCCTGCCCCG

P_AAX80056 361 GCCGGGCCTGCAGCTCCTGGACCTGTCACAGAACCAGATCGCCAGCCTGCGCCTGCCCCG

DNA44804 421 CCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCGGCATCCTGGA

P_AAX80056 421 CCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCGGCATCCTGGA

DNA44804 481 CACTGCCAACGTGGAGGCGCTGCGGCTGGCTGGTCTGGGGCTGCAGCAGCTGGACGAGGG

P_AAX80056 481 CACTGCCAACGTGGAGGCGCTGCGGCTGGCTGGTCTGGGGCTGCAGCAGCTGGACGAGGG

DNA44804 541 GCTCTTCAGCCGCTTGCGCAACCTCCACGACCTGGATGTGTCCGACAACCAGCTGGAGCG

P_AAX80056 541 GCTCTTCAGCCGCTTGCGCAACCTCCACGACCTGGATGTGTCCGACAACCAGCTGGAGCG

DNA44804 601 AGTGCCACCTGTGATCCGAGGCCTCCGGGGCCTGACGCGCCTGCGGCTGGCCGGCAACAC

P_AAX80056 601 AGTGCCACCTGTGATCCGAGGCCTCCGGGGCCTGACGCGCCTGCGGCTGGCCGGCAACAC

DNA44804 661 CCGCATTGCCAGCTGCGGCCCCGAGGACCTGGCCGGCCTGGCTGCCCTGCAGGAGCTGGA

P_AAX80056 661 CCGCATTGCCAGCTGCGGCCCCGAGGACCTGGCCGGCCTGGCTGCCCTGCAGGAGCTGGA

DNA44804 721 TGTGAGCAACCTAAGCCTGCAGGCCCTGCCTGGCGACCTCTCGGGCCTCTCCCCCGCCT

P_AAX80056 721 TGTGAGCAACCTAAGCCTGCAGGCCCTGCCTGGCGACCTCTCGGGCCTCTCCCCCGCCT

DNA44804 781 GCGGCTGCTGGCAGCTGCCCCGAACCCCTTCAACTGCGTGTGCCCCCTGAGCTGGTTTGG

P_AAX80056 781 GCGGCTGCTGGCAGCTGCCCCGAACCCCTTCAACTGCGTGTGCCCCCTGAGCTGGTTTGG

DNA44804 841 CCCCTGGGTGCGCGAGAGCCACGTCACTGGCCAGCCCTGAGGAGACGCGCTGCCACTT

P_AAX80056 841 CCCCTGGGTGCGCGAGAGCCACGTCACTGGCCAGCCCTGAGGAGACGCGCTGCCACTT

DNA44804 901 CCCGCCCAAGAACGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCCGACTTTGGCTGCCC

P_AAX80056 901 CCCGCCCAAGAACGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCCGACTTTGGCTGCCC

DNA44804 961 AGCCACCACCACCACAGCCACAGTGCCACCACGAGGCCCGTGGTGCGGGAGCCACAGC

P_AAX80056 961 AGCCACCACCACCACAGCCACAGTGCCACCACGAGGCCCGTGGTGCGGGAGCCACAGC

DNA44804 1021 CTTGTCTTCTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCGGCCACTGAGGCCCC

P_AAX80056 1021 CTTGTCTTCTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCGGCCACTGAGGCCCC

DNA44804 1081 CAGCCCGCCCTCCACTGCCCCACCGACTGTAGGGCCTGTCCCCCAGCCCCAGGACTGCCC

P_AAX80056 1081 CAGCCCGCCCTCCACTGCCCCACCGACTGTAGGGCCTGTCCCCCAGCCCCAGGACTGCCC

DNA44804 1141 ACCGTCCACCTGCCTCAATGGGGGCACATGCCACCTGGGGACACGGCACCACCTGGCGTG

P_AAX80056 1141 ACCGTCCACCTGCCTCAATGGGGGCACATGCCACCTGGGGACACGGCACCACCTGGCGTG

BUAST RESULTS A-B

DNA44804	1201	CTTGTGCCCCGAAGGCTTCACGGGCCTGTACTGTGAGAGCCAGATGGGGCAGGGGACACG
P_AAX80056	1201	CTTGTGCCCCGAAGGCTTCACGGGCCTGTACTGTGAGAGCCAGATGGGGCAGGGGACACG
DNA44804	1261	CCCCAGCCCTACACCAGTCACGCCGAGGCCACCACGGTCCCTGACCCTGGGCATCGAGCC
P_AAX80056	1261	CCCCAGCCCTACACCAGTCACGCCGAGGCCACCACGGTCCCTGACCCTGGGCATCGAGCC
DNA44804	1321	GGTGAGCCCCACCTCCCTGCGCGTGGGGCTGCAGCGCTACCTCCAGGGGAGCTCCGTGCA
P_AAX80056	1321	GGTGAGCCCCACCTCCCTGCGCGTGGGGCTGCAGCGCTACCTCCAGGGGAGCTCCGTGCA
DNA44804	1381	GCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCGGGCCCTGATAAGCGGCTGGTGAC
P_AAX80056	1381	GCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCGGGCCCTGATAAGCGGCTGGTGAC
DNA44804	1441	GCTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTCACCCAGCTGCGGCCCAACGCCAC
P_AAX80056	1441	GCTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTCACCCAGCTGCGGCCCAACGCCAC
DNA44804	1501	TTACTCCGTCTGTGTCATGCCTTTGGGGCCCGGGCGGGTGCCGGAGGGCGAGGAGGCCTG
P_AAX80056	1501	TTACTCCGTCTGTGTCATGCCTTTGGGGCCCGGGCGGGTGCCGGAGGGCGAGGAGGCCTG
DNA44804	1561	CGGGGAGGCCCATACACCCCAAGCCGTCCACTCCAACCACGCCCCAGTCACCCAGGCCCG
P_AAX80056	1561	CGGGGAGGCCCATACACCCCAAGCCGTCCACTCCAACCACGCCCCAGTCACCCAGGCCCG
DNA44804	1621	CGAGGGCAACCTGCCGCTCCTCATTCGCGCCCGCCCTGGCCGCGGTGCTCCTGGCCGCGCT
P_AAX80056	1621	CGAGGGCAACCTGCCGCTCCTCATTCGCGCCCGCCCTGGCCGCGGTGCTCCTGGCCGCGCT
DNA44804	1681	GGCTGCGGTGGGGGCAGCCTACTGTGTGCGGCGGGGGCGGGCCATGGCAGCAGCGGCTCA
P_AAX80056	1681	GGCTGCGGTGGGGGCAGCCTACTGTGTGCGGCGGGGGCGGGCCATGGCAGCAGCGGCTCA
DNA44804	1741	GGACAAAGGGCAGGTGGGGCCAGGGGCTGGGCCCTGGAAGTGGAGGGAGTGAAGGTCCC
P_AAX80056	1741	GGACAAAGGGCAGGTGGGGCCAGGGGCTGGGCCCTGGAAGTGGAGGGAGTGAAGGTCCC
DNA44804	1801	CTTGAGCCAGGCCCCAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCAGCGGGTCTGA
P_AAX80056	1801	CTTGAGCCAGGCCCCAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCAGCGGGTCTGA
DNA44804	1861	GTGTGAGGTGCCACTCATGGGCTTCCCAGGGCCTGGCCTCCAGTCACCCCTCCACGCAAA
P_AAX80056	1861	GTGTGAGGTGCCACTCATGGGCTTCCCAGGGCCTGGCCTCCAGTCACCCCTCCACGCAAA
DNA44804	1921	GCCCTACATCTAAGCCAGAGAGAGACAGGGCAGCTGGGGCCGGGCTCTCAGCCAGTGAGA
P_AAX80056	1921	GCCCTACATCTAAGCCAGAGAGAGACAGGGCAGCTGGGGCCGGGCTCTCAGCCAGTGAGA
DNA44804	1981	TGGCCAGCCCCCTCCTGCTGCCACACCACGTAAGTTCTCAGTCCCAACCTCGGGGATGTG
P_AAX80056	1981	TGGCCAGCCCCCTCCTGCTGCCACACCACGTAAGTTCTCAGTCCCAACCTCGGGGATGTG

BLAST RESULTS A-9

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DNA44804 2041 TGCAGACAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGACCTCGGTCTCCTCA
*****
P_AAX80056 2041 TGCAGACAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGACCTCGGTCTCCTCA

DNA44804 2101 TCTGTGAGATGCTGTGGCCCAGCTGACGAGCCCTAACGTCCCCAGAACCAGTGCCTATG
*****
P_AAX80056 2101 TCTGTGAGATGCTGTGGCCCAGCTGACGAGCCCTAACGTCCCCAGAACCAGTGCCTATG

DNA44804 2161 AGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCACGGCGGGCCCTGCCA
*****
P_AAX80056 2161 AGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCACGGCGGGCCCTGCCA

DNA44804 2221 TGTGCTGGTAACGCATGCCTGGGCCCTGCTGGGCTCTCCCACTCCAGGCGGACCCTGGGG
*****
P_AAX80056 2221 TGTGCTGGTAACGCATGCCTGGGCCCTGCTGGGCTCTCCCACTCCAGGCGGACCCTGGGG

DNA44804 2281 GCCAGTGAAGGAAGCTCCCGGAAAGAGCAGAGGGAGAGCGGGTAGGCGGCTGTGTGACTC
*****
P_AAX80056 2281 GCCAGTGAAGGAAGCTCCCGGAAAGAGCAGAGGGAGAGCGGGTAGGCGGCTGTGTGACTC

DNA44804 2341 TAGTCTTGGCCCCAGGAAGCGAAGGAACAAAAGAACTGGAAAGGAAGATGCTTTAGGAA
*****
P_AAX80056 2341 TAGTCTTGGCCCCAGGAAGCGAAGGAACAAAAGAACTGGAAAGGAAGATGCTTTAGGAA

DNA44804 2401 CATGTTTTGCTTTTTTAAATATATATATATTTATAAGAGATCCTTTCCATTATTCTG
*****
P_AAX80056 2401 CATGTTTTGCTTTTTTAAATATATATATATTTATAAGAGATCCTTTCCATTATTCTG

DNA44804 2461 GGAAGATGTTTTTCAAACCTCAGAGACAAGGACTTTGGTTTTTGTAAAGACAAACGATGATA
*****
P_AAX80056 2461 GGAAGATGTTTTTCAAACCTCAGAGACAAGGACTTTGGTTTTTGTAAAGACAAACGATGATA

DNA44804 2521 TGAAGGCCTTTTGTAAAGAAAAATAAAAAAAAAA
*****
P_AAX80056 2521 TGAAGGCCTTTTGTAAAGAAAAATAAAAAAAAAA

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>4 P_AAX87261 cDNA clone encoding human PRO357, amplified in tumour cells. (2555 bp) [1 seg]
Score = 2555 (5065 bits), Expect = 0.0
Identities = 2555/2555 (100%), at 1,1-2555,2555, Strand +/+

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DNA44804 1 GGGGCGGGTGGACGCGGACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCC
*****
P_AAX87261 1 GGGGCGGGTGGACGCGGACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCC

DNA44804 61 GACCCGCCAGGAAAGACTGAGGCCGCGGCCTGCCCGCCCGGCTCCCTGCGCCGCCGCCG
*****
P_AAX87261 61 GACCCGCCAGGAAAGACTGAGGCCGCGGCCTGCCCGCCCGGCTCCCTGCGCCGCCGCCG

DNA44804 121 CCTCCCGGGACAGAAGATGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACT
*****
P_AAX87261 121 CCTCCCGGGACAGAAGATGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACT

DNA44804 181 GGCCCTGGGGCCTGGGGTGCAGGGCTGCCCATCCGGTGCCAGTGCAGCCAGCCACAGAC
*****
P_AAX87261 181 GGCCCTGGGGCCTGGGGTGCAGGGCTGCCCATCCGGTGCCAGTGCAGCCAGCCACAGAC

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BLAST RESULTS A-14

DNA44804	241	AGTCTTCTGCACTGCCCCGCCAGGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGT

P_AAX87261	241	AGTCTTCTGCACTGCCCCGCCAGGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGT
DNA44804	301	GGGGCTGTACGTCTTTGAGAACGGCATCACCATGCTCGACGCAAGCAGCTTTGCCGGCCT

P_AAX87261	301	GGGGCTGTACGTCTTTGAGAACGGCATCACCATGCTCGACGCAAGCAGCTTTGCCGGCCT
DNA44804	361	GCCGGGCCTGCAGCTCCTGGACCTGTACAGAACCAGATCGCCAGCCTGCGCCTGCCCCG

P_AAX87261	361	GCCGGGCCTGCAGCTCCTGGACCTGTACAGAACCAGATCGCCAGCCTGCGCCTGCCCCG
DNA44804	421	CCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCGGCATCCTGGA

P_AAX87261	421	CCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCGGCATCCTGGA
DNA44804	481	CACTGCCAACGTGGAGGCGCTGCGGCTGGCTGGTCTGGGGCTGCAGCAGCTGGACGAGGG

P_AAX87261	481	CACTGCCAACGTGGAGGCGCTGCGGCTGGCTGGTCTGGGGCTGCAGCAGCTGGACGAGGG
DNA44804	541	GCTCTTCAGCCGCTTGCGCAACCTCCACGACCTGGATGTGTCCGACAACCAGCTGGAGCG

P_AAX87261	541	GCTCTTCAGCCGCTTGCGCAACCTCCACGACCTGGATGTGTCCGACAACCAGCTGGAGCG
DNA44804	601	AGTGCCACCTGTGATCCGAGGCCTCCGGGGCCTGACGCGCCTGCGGCTGGCCGGCAACAC

P_AAX87261	601	AGTGCCACCTGTGATCCGAGGCCTCCGGGGCCTGACGCGCCTGCGGCTGGCCGGCAACAC
DNA44804	661	CCGCATTGCCCAGCTGCGGCCCGAGGACCTGGCCGGCCTGGCTGCCCTGCAGGAGCTGGA

P_AAX87261	661	CCGCATTGCCCAGCTGCGGCCCGAGGACCTGGCCGGCCTGGCTGCCCTGCAGGAGCTGGA
DNA44804	721	TGTGAGCAACCTAAGCCTGCAGGCCCTGCCTGGCGACCTCTCGGGCCTCTTCCCCCGCCT

P_AAX87261	721	TGTGAGCAACCTAAGCCTGCAGGCCCTGCCTGGCGACCTCTCGGGCCTCTTCCCCCGCCT
DNA44804	781	GCGGCTGCTGGCAGCTGCCCCGCAACCCCTTCAACTGCGTGTGCCCCCTGAGCTGGTTTGG

P_AAX87261	781	GCGGCTGCTGGCAGCTGCCCCGCAACCCCTTCAACTGCGTGTGCCCCCTGAGCTGGTTTGG
DNA44804	841	CCCCTGGGTGCGCGAGAGCCACGTCACTGGCCAGCCCTGAGGAGACGCGCTGCCACTT

P_AAX87261	841	CCCCTGGGTGCGCGAGAGCCACGTCACTGGCCAGCCCTGAGGAGACGCGCTGCCACTT
DNA44804	901	CCCGCCCAAGAACGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCCGACTTTGGCTGCCC

P_AAX87261	901	CCCGCCCAAGAACGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCCGACTTTGGCTGCCC
DNA44804	961	AGCCACCACCACCACAGCCACAGTGCCCACCACGAGGCCCGTGGTGCGGGAGCCACAGC

P_AAX87261	961	AGCCACCACCACCACAGCCACAGTGCCCACCACGAGGCCCGTGGTGCGGGAGCCACAGC
DNA44804	1021	CTTGTCTTCTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCGGCCACTGAGGCCCC

P_AAX87261	1021	CTTGTCTTCTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCGGCCACTGAGGCCCC
DNA44804	1081	CAGCCCGCCCTCCACTGCCCCACCGACTGTAGGGCCTGTCCCCCAGCCCCAGGACTGCCC

BLAST RESULTS A-11

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*****
P_AAX87261 1081 CAGCCCGCCCTCCACTGCCCCACCGACTGTAGGGCCTGTCCCCCAGCCCCAGGACTGCC
DNA44804 1141 ACCGTCCACCTGCCTCAATGGGGGCACATGCCACCTGGGGACACGGCACCACCTGGCGTG
*****
P_AAX87261 1141 ACCGTCCACCTGCCTCAATGGGGGCACATGCCACCTGGGGACACGGCACCACCTGGCGTG
DNA44804 1201 CTTGTGCCCCGAAGGCTTCACGGGCCTGTACTGTGAGAGCCAGATGGGGCAGGGGACACG
*****
P_AAX87261 1201 CTTGTGCCCCGAAGGCTTCACGGGCCTGTACTGTGAGAGCCAGATGGGGCAGGGGACACG
DNA44804 1261 GCCCAGCCCTACACCAGTCACGCCGAGGCCACCACGGTCCCTGACCCTGGGCATCGAGCC
*****
P_AAX87261 1261 GCCCAGCCCTACACCAGTCACGCCGAGGCCACCACGGTCCCTGACCCTGGGCATCGAGCC
DNA44804 1321 GGTGAGCCCCACCTCCCTGCGCGTGGGGCTGCAGCGCTACCTCCAGGGGAGCTCCGTGCA
*****
P_AAX87261 1321 GGTGAGCCCCACCTCCCTGCGCGTGGGGCTGCAGCGCTACCTCCAGGGGAGCTCCGTGCA
DNA44804 1381 GCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCGGGCCCTGATAAGCGGCTGGTGAC
*****
P_AAX87261 1381 GCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCGGGCCCTGATAAGCGGCTGGTGAC
DNA44804 1441 GCTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTCACCCAGCTGCGGCCCAACGCCAC
*****
P_AAX87261 1441 GCTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTCACCCAGCTGCGGCCCAACGCCAC
DNA44804 1501 TTACTCCGTCTGTGTCATGCCTTTGGGGCCCGGGCGGGTGCCCGAGGGCGAGGAGGCCTG
*****
P_AAX87261 1501 TTACTCCGTCTGTGTCATGCCTTTGGGGCCCGGGCGGGTGCCCGAGGGCGAGGAGGCCTG
DNA44804 1561 CGGGGAGGCCCATACACCCCCAGCCGTCCACTCCAACCACGCCCCAGTCACCCAGGCCCCG
*****
P_AAX87261 1561 CGGGGAGGCCCATACACCCCCAGCCGTCCACTCCAACCACGCCCCAGTCACCCAGGCCCCG
DNA44804 1621 CGAGGGCAACCTGCCGCTCCTCATTGCGCCCGCCCTGGCCGCGGTGCTCCTGGCCGCGCT
*****
P_AAX87261 1621 CGAGGGCAACCTGCCGCTCCTCATTGCGCCCGCCCTGGCCGCGGTGCTCCTGGCCGCGCT
DNA44804 1681 GGCTGCGGTGGGGGCAGCCTACTGTGTGCGGCGGGGCGGGCCATGGCAGCAGCGGCTCA
*****
P_AAX87261 1681 GGCTGCGGTGGGGGCAGCCTACTGTGTGCGGCGGGGCGGGCCATGGCAGCAGCGGCTCA
DNA44804 1741 GGACAAAGGGCAGGTGGGGCCAGGGGCTGGGCCCTGGAAGTGGAGGGAGTGAAGGTCCC
*****
P_AAX87261 1741 GGACAAAGGGCAGGTGGGGCCAGGGGCTGGGCCCTGGAAGTGGAGGGAGTGAAGGTCCC
DNA44804 1801 CTTGGAGCCAGGCCCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCAGCGGGTCTGA
*****
P_AAX87261 1801 CTTGGAGCCAGGCCCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCAGCGGGTCTGA
DNA44804 1861 GTGTGAGGTGCCACTCATGGGCTTCCAGGGCCTGGCCTCCAGTACCCCTCCACGCAA
*****
P_AAX87261 1861 GTGTGAGGTGCCACTCATGGGCTTCCAGGGCCTGGCCTCCAGTACCCCTCCACGCAA
DNA44804 1921 GCCCTACATCTAAGCCAGAGAGACAGGGCAGCTGGGGCCGGGCTCTCAGCCAGTGAGA
*****

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BLAST RESULTS A-12

P_AAX87261 1921 GCCCTACATCTAAGCCAGAGAGACAGGGCAGCTGGGGCCGGGCTCTCAGCCAGTGAGA
DNA44804 1981 TGGCCAGCCCCCTCCTGCTGCCACACCACGTAAGTTCTCAGTCCCAACCTCGGGGATGTG

P_AAX87261 1981 TGGCCAGCCCCCTCCTGCTGCCACACCACGTAAGTTCTCAGTCCCAACCTCGGGGATGTG
DNA44804 2041 TGCAGACAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGACCTCGGTCTCCTCA

P_AAX87261 2041 TGCAGACAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGACCTCGGTCTCCTCA
DNA44804 2101 TCTGTGAGATGCTGTGGCCCAGCTGACGAGCCCTAACGTCCCCAGAACCGAGTGCCTATG

P_AAX87261 2101 TCTGTGAGATGCTGTGGCCCAGCTGACGAGCCCTAACGTCCCCAGAACCGAGTGCCTATG
DNA44804 2161 AGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCACGGCGGGCCCTGCCA

P_AAX87261 2161 AGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCACGGCGGGCCCTGCCA
DNA44804 2221 TGTGCTGGTAACGCATGCCTGGGCCCTGCTGGGCTCTCCCACTCCAGGCGGACCCTGGGG

P_AAX87261 2221 TGTGCTGGTAACGCATGCCTGGGCCCTGCTGGGCTCTCCCACTCCAGGCGGACCCTGGGG
DNA44804 2281 GCCAGTGAAGGAAGCTCCCGAAAGAGCAGAGGGAGAGCGGGTAGGCGGCTGTGTGACTC

P_AAX87261 2281 GCCAGTGAAGGAAGCTCCCGAAAGAGCAGAGGGAGAGCGGGTAGGCGGCTGTGTGACTC
DNA44804 2341 TAGTCTTGGCCCCAGGAAGCGAAGGAACAAAAGAACTGGAAAGGAAGATGCTTTAGGAA

P_AAX87261 2341 TAGTCTTGGCCCCAGGAAGCGAAGGAACAAAAGAACTGGAAAGGAAGATGCTTTAGGAA
DNA44804 2401 CATGTTTTGCTTTTTTAAATATATATATATTTATAAGAGATCCTTTCCCATTTATTCTG

P_AAX87261 2401 CATGTTTTGCTTTTTTAAATATATATATATTTATAAGAGATCCTTTCCCATTTATTCTG
DNA44804 2461 GGAAGATGTTTTTCAAACCTCAGAGACAAGGACTTTGGTTTTTGTAGACAAACGATGATA

P_AAX87261 2461 GGAAGATGTTTTTCAAACCTCAGAGACAAGGACTTTGGTTTTTGTAGACAAACGATGATA
DNA44804 2521 TGAAGGCCTTTTGTAGAAAAAATAAAAAAAAAAA

P_AAX87261 2521 TGAAGGCCTTTTGTAGAAAAAATAAAAAAAAAAA

>5 P_AAA58765 cDNA encoding a leucine-rich surface glycoprotein (LRSG). (2852 bp) [2 segs]

Score = 2142 (4246 bits), Expect = 0.0 [P_AAA58765, seg 1/2]

Identities = 2142/2142 (100%), at 407,655-2548,2796, Strand +/-

DNA44804 407 CTGCGCCTGCCCCGCCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAG

P_AAA58765 655 CTGCGCCTGCCCCGCCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAG
DNA44804 467 CCCGGCATCCTGGACACTGCCAACGTGGAGGCGCTGCGGCTGGCTGGTCTGGGGCTGCAG

P_AAA58765 715 CCCGGCATCCTGGACACTGCCAACGTGGAGGCGCTGCGGCTGGCTGGTCTGGGGCTGCAG
DNA44804 527 CAGCTGGACGAGGGGCTCTTCAGCCGCTTGC GCAACCTCCACGACCTGGATGTGTCCGAC

BLAST RESULTS A-13

P_AAA58765 775 CAGCTGGACGAGGGGCTCTTCAGCCGCTTGCGCAACCTCCACGACCTGGATGTGTCCGAC

DNA44804 587 AACCAGCTGGAGCGAGTGCCACCTGTGATCCGAGGCCTCCGGGGCCTGACGCGCCTGCGG

P_AAA58765 835 AACCAGCTGGAGCGAGTGCCACCTGTGATCCGAGGCCTCCGGGGCCTGACGCGCCTGCGG

DNA44804 647 CTGGCCGGCAACACCCGCATTGCCCAGCTGCGGCCCGAGGACCTGGCCGGCCTGGCTGCC

P_AAA58765 895 CTGGCCGGCAACACCCGCATTGCCCAGCTGCGGCCCGAGGACCTGGCCGGCCTGGCTGCC

DNA44804 707 CTGCAGGAGCTGGATGTGAGCAACCTAAGCCTGCAGGCCCTGCCTGGCGACCTCTCGGGC

P_AAA58765 955 CTGCAGGAGCTGGATGTGAGCAACCTAAGCCTGCAGGCCCTGCCTGGCGACCTCTCGGGC

DNA44804 767 CTCTTCCCCCGCCTGCGGGTGCTGGCAGCTGCCCCGAACCCCTTCAACTGCGTGTGCCCC

P_AAA58765 1015 CTCTTCCCCCGCCTGCGGGTGCTGGCAGCTGCCCCGAACCCCTTCAACTGCGTGTGCCCC

DNA44804 827 CTGAGCTGGTTTGGCCCCCTGGGTGCGCGAGAGCCACGTCACTAGGCCAGCCCTGAGGAG

P_AAA58765 1075 CTGAGCTGGTTTGGCCCCCTGGGTGCGCGAGAGCCACGTCACTAGGCCAGCCCTGAGGAG

DNA44804 887 ACGCGCTGCCACTTCCCGCCCAAGAACGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCC

P_AAA58765 1135 ACGCGCTGCCACTTCCCGCCCAAGAACGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCC

DNA44804 947 GACTTTGGCTGCCCAGCCACCACCACAGCCACAGTGCCCACCACGAGGCCCGTGGTG

P_AAA58765 1195 GACTTTGGCTGCCCAGCCACCACCACAGCCACAGTGCCCACCACGAGGCCCGTGGTG

DNA44804 1007 CGGGAGCCACAGCCTTGCTTCTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCG

P_AAA58765 1255 CGGGAGCCACAGCCTTGCTTCTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCG

DNA44804 1067 GCCACTGAGGCCCCCAGCCCGCCCTCCACTGCCCCACCGACTGTAGGGCCTGTCCCCCAG

P_AAA58765 1315 GCCACTGAGGCCCCCAGCCCGCCCTCCACTGCCCCACCGACTGTAGGGCCTGTCCCCCAG

DNA44804 1127 CCCCAGGACTGCCCACCGTCCACCTGCCTCAATGGGGGCACATGCCACCTGGGGACACGG

P_AAA58765 1375 CCCCAGGACTGCCCACCGTCCACCTGCCTCAATGGGGGCACATGCCACCTGGGGACACGG

DNA44804 1187 CACCACCTGGCGTGCTTGTGCCCCGAAGGCTTCACGGGCCTGTACTGTGAGAGCCAGATG

P_AAA58765 1435 CACCACCTGGCGTGCTTGTGCCCCGAAGGCTTCACGGGCCTGTACTGTGAGAGCCAGATG

DNA44804 1247 GGGCAGGGGACACGGCCAGCCCTACACCAGTCACGCCGAGGCCACCACGGTCCCTGACC

P_AAA58765 1495 GGGCAGGGGACACGGCCAGCCCTACACCAGTCACGCCGAGGCCACCACGGTCCCTGACC

DNA44804 1307 CTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGCGTGGGGCTGCAGCGCTACCTCCAG

P_AAA58765 1555 CTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGCGTGGGGCTGCAGCGCTACCTCCAG

DNA44804 1367 GGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCGGGCCCTGAT

P_AAA58765 1615 GGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCGGGCCCTGAT

BLAST RESULTS A-14

DNA44804	1427	AAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTCACCCAGCTG

P_AAA58765	1675	AAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTCACCCAGCTG
DNA44804	1487	CGGCCCAACGCCACTTACTCCGTCTGTGTCATGCCTTTGGGGCCCCGGGCGGGTGCCGGAG

P_AAA58765	1735	CGGCCCAACGCCACTTACTCCGTCTGTGTCATGCCTTTGGGGCCCCGGGCGGGTGCCGGAG
DNA44804	1547	GGCGAGGAGGCCTGCGGGGAGGCCCATACACCCCGAGCCGTCCACTCCAACCACGCCCCA

P_AAA58765	1795	GGCGAGGAGGCCTGCGGGGAGGCCCATACACCCCGAGCCGTCCACTCCAACCACGCCCCA
DNA44804	1607	GTCACCCAGGCCCGCGAGGGCAACCTGCCGCTCCTCATTGCGCCCCGCCCTGGCCGCGGTG

P_AAA58765	1855	GTCACCCAGGCCCGCGAGGGCAACCTGCCGCTCCTCATTGCGCCCCGCCCTGGCCGCGGTG
DNA44804	1667	CTCCTGGCCGCGCTGGCTGCGGTGGGGGCAGCCTACTGTGTGCGGCGGGGGCGGGCCATG

P_AAA58765	1915	CTCCTGGCCGCGCTGGCTGCGGTGGGGGCAGCCTACTGTGTGCGGCGGGGGCGGGCCATG
DNA44804	1727	GCAGCAGCGGCTCAGGACAAAGGGCAGGTGGGGCCAGGGGCTGGGCCCTGGAACTGGAG

P_AAA58765	1975	GCAGCAGCGGCTCAGGACAAAGGGCAGGTGGGGCCAGGGGCTGGGCCCTGGAACTGGAG
DNA44804	1787	GGAGTGAAGGTCCCCTTGGAGCCAGGCCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTG

P_AAA58765	2035	GGAGTGAAGGTCCCCTTGGAGCCAGGCCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTG
DNA44804	1847	CCCAGCGGGTCTGAGTGTGAGGTGCCACTCATGGGCTTCCCAGGGCCTGGCCTCCAGTCA

P_AAA58765	2095	CCCAGCGGGTCTGAGTGTGAGGTGCCACTCATGGGCTTCCCAGGGCCTGGCCTCCAGTCA
DNA44804	1907	CCCCTCCACGCAAAGCCCTACATCTAAGCCAGAGAGAGACAGGGCAGCTGGGGCCGGGCT

P_AAA58765	2155	CCCCTCCACGCAAAGCCCTACATCTAAGCCAGAGAGAGACAGGGCAGCTGGGGCCGGGCT
DNA44804	1967	CTCAGCCAGTGAGATGGCCAGCCCCCTCCTGCTGCCACACCACGTAAGTTCTCAGTCCCA

P_AAA58765	2215	CTCAGCCAGTGAGATGGCCAGCCCCCTCCTGCTGCCACACCACGTAAGTTCTCAGTCCCA
DNA44804	2027	ACCTCGGGGATGTGTGCAGACAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGA

P_AAA58765	2275	ACCTCGGGGATGTGTGCAGACAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGA
DNA44804	2087	CCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCCAGCTGACGAGCCCTAACGTCCCCAGA

P_AAA58765	2335	CCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCCAGCTGACGAGCCCTAACGTCCCCAGA
DNA44804	2147	ACCGAGTGCTATGAGGACAGTGTCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCAC

P_AAA58765	2395	ACCGAGTGCTATGAGGACAGTGTCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCAC
DNA44804	2207	GGCGGGCCCTGCCATGTGCTGGTAACGCATGCCTGGGCCCTGCTGGGCTCTCCCACTCCA

P_AAA58765	2455	GGCGGGCCCTGCCATGTGCTGGTAACGCATGCCTGGGCCCTGCTGGGCTCTCCCACTCCA

BLAST RESULTS A-B

DNA44804 2267 GGCGGACCCTGGGGGCCAGTGAAGGAAGCTCCCGGAAAGAGCAGAGGGAGAGCGGGTAGG

 P_AAA58765 2515 GGCGGACCCTGGGGGCCAGTGAAGGAAGCTCCCGGAAAGAGCAGAGGGAGAGCGGGTAGG
 DNA44804 2327 CGGCTGTGTGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAAGAACTGGAAAGGA

 P_AAA58765 2575 CGGCTGTGTGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAAGAACTGGAAAGGA
 DNA44804 2387 AGATGCTTTAGGAACATGTTTTGCTTTTTTAAATATATATATATTTATAAGAGATCCTT

 P_AAA58765 2635 AGATGCTTTAGGAACATGTTTTGCTTTTTTAAATATATATATATTTATAAGAGATCCTT
 DNA44804 2447 TCCCATTTATTCTGGGAAGATGTTTTTCAAACCTCAGAGACAAGGACTTTGGTTTTGTAA

 P_AAA58765 2695 TCCCATTTATTCTGGGAAGATGTTTTTCAAACCTCAGAGACAAGGACTTTGGTTTTGTAA
 DNA44804 2507 GACAAACGATGATATGAAGGCCTTTTGTAGAAAAAATAAAA

 P_AAA58765 2755 GACAAACGATGATATGAAGGCCTTTTGTAGAAAAAATAAAA

Score = 406 (805 bits), Expect = 0.0 [P_AAA58765, seg 2/2]
 Identities = 409/410 (99%), at 1,24-410,433, Strand +/-

DNA44804 1 GGGGCGGGTGGACGCGGACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCC

 P_AAA58765 24 GGGGCGGGTGGACGCGGACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCC
 DNA44804 61 GACCCGCCAGGAAAGACTGAGGCCGCGGCCTGCCCCGCCCGGCTCCCTGCGCCGCCGCCG

 P_AAA58765 84 GACCCGCCAGGAAAGACTGAGGCCGCGGCCTGCCCCGCCCGGCTCCCTGCGCCGCCGCCG
 DNA44804 121 CCTCCCGGGACAGAAGATGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACT

 P_AAA58765 144 CCTCCCGGGACAGAAGATGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACT
 DNA44804 181 GGCCCTGGGGCCTGGGGTGCAGGGCTGCCCATCCGGCTGCCAGTGCAGCCAGCCACAGAC

 P_AAA58765 204 GGCCCTGGGGCCTGGGGTGCAGGGCTGCCCATCCGGCTGCCAGTGCAGCCAGCCACAGAC
 DNA44804 241 AGTCTTCTGCACTGCCCCGCCAGGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGT

 P_AAA58765 264 AGTCTTCTGCACTGCCCCGCCAGGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGT
 DNA44804 301 GGGGCTGTACGTCTTTGAGAACGGCATCACCATGCTCGACGCAAGCAGCTTTGCCGGCCT

 P_AAA58765 324 GGGGCTGTACGTCTTTGAGAACGGCATCACCATGCTCGACGCAAGCAGCTTTGCCGGCCT
 DNA44804 361 GCCGGGCCTGCAGCTCCTGGACCTGTCACAGAACCAGATCGCCAGCCTGC

 P_AAA58765 384 GCCGGGCCTGCAGCTCCTGGACCTGTCACAGAACCAGATCGCCAGCCTGC

>6 AC012676 Homo sapiens chromosome 16 clone RP11-295D4, WORKING DRAFT (172139 bp) [3 segs]

Score = 2138 (4238 bits), Expect = 0.0 [AC012676, seg 1/3]
 Identities = 2141/2142 (99%), at 407,81365-2548,83506, Strand +/-

DNA44804 407 CTGCGCCTGCCCCGCCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAG

BLAST RESULTS A-14


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*****
AC012676 81365 CTGCGCCTGCCCCGCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAG
DNA44804 467 CCCGGCATCCTGGACACTGCCAACGTGGAGGCGCTGCGGCTGGCTGGTCTGGGGCTGCAG
*****
AC012676 81425 CCCGGCATCCTGGACACTGCCAACGTGGAGGCGCTGCGGCTGGCTGGTCTGGGGCTGCAG
DNA44804 527 CAGCTGGACGAGGGGCTCTTCAGCCGCTTGCGCAACCTCCACGACCTGGATGTGTCCGAC
*****
AC012676 81485 CAGCTGGACGAGGGGCTCTTCAGCCGCTTGCGCAACCTCCACGACCTGGATGTGTCCGAC
DNA44804 587 AACCAGCTGGAGCGAGTGCCACCTGTGATCCGAGGCCTCCGGGGCCTGACGCGCCTGCGG
*****
AC012676 81545 AACCAGCTGGAGCGAGTGCCACCTGTGATCCGAGGCCTCCGGGGCCTGACGCGCCTGCGG
DNA44804 647 CTGGCCGGCAACACCCGCATTGCCCAGCTGCGGCCCGAGGACCTGGCCGGCCTGGCTGCC
*****
AC012676 81605 CTGGCCGGCAACACCCGCATTGCCCAGCTGCGGCCCGAGGACCTGGCCGGCCTGGCTGCC
DNA44804 707 CTGCAGGAGCTGGATGTGAGCAACCTAAGCCTGCAGGCCCTGCCTGGCGACCTCTCGGGC
*****
AC012676 81665 CTGCAGGAGCTGGATGTGAGCAACCTAAGCCTGCAGGCCCTGCCTGGCGACCTCTCGGGC
DNA44804 767 CTCTTCCCCCGCCTGCGGCTGCTGGCAGCTGCCCAGCAACCCCTTCAACTGCGTGTGCCCC
*****
AC012676 81725 CTCTTCCCCCGCCTGCGGCTGCTGGCAGCTGCCCAGCAACCCCTTCAACTGCGTGTGCCCC
DNA44804 827 CTGAGCTGGTTTGGCCCTGGGTGCGCGAGAGCCACGTCACTAGGCCAGCCCTGAGGAG
*****
AC012676 81785 CTGAGCTGGTTTGGCCCTGGGTGCGCGAGAGCCACGTCACTAGGCCAGCCCTGAGGAG
DNA44804 887 ACGCGCTGCCACTTCCCGCCCAAGAACGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCC
*****
AC012676 81845 ACGCGCTGCCACTTCCCGCCCAAGAACGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCC
DNA44804 947 GACTTTGGCTGCCCAGCCACCACCACACAGCCACAGTGCCCAACACGAGGCCCGTGGTG
*****
AC012676 81905 GACTTTGGCTGCCCAGCCACCACCACACAGCCACAGTGCCCAACACGAGGCCCGTGGTG
DNA44804 1007 CGGGAGCCACAGCCTTGTCTTCTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCG
*****
AC012676 81965 CGGGAGCCACAGCCTTGTCTTCTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGAGCCG
DNA44804 1067 GCCACTGAGGCCCCCAGCCCGCCCTCCACTGCCCCACCGACTGTAGGGCCTGTCCCCCAG
*****
AC012676 82025 GCCACTGAGGCCCCCAGCCCGCCCTCCACTGCCCCACCGACTGTAGGGCCTGTCCCCCAG
DNA44804 1127 CCCCAGGACTGCCACCGTCCACCTGCCTCAATGGGGGCACATGCCACCTGGGGACACGG
*****
AC012676 82085 CCCCAGGACTGCCACCGTCCACCTGCCTCAATGGGGGCACATGCCACCTGGGGACACGG
DNA44804 1187 CACCACCTGGCGTGCTTGTGCCCCGAAGGCTTCACGGGCCTGTACTGTGAGAGCCAGATG
*****
AC012676 82145 CACCACCTGGCGTGCTTGTGCCCCGAAGGCTTCACGGGCCTGTACTGTGAGAGCCAGATG
DNA44804 1247 GGGCAGGGGACACGGCCAGCCCTACACCAGTCACGCCGAGGCCACCACGGTCCCTGACC
*****

```

BLAST RESULTS A-17

AC012676	82205	GGGCAGGGGACACGGCCCCAGCCCTACACCAGTCACGCCGAGGCCACCACGGTCCCTGACC
DNA44804	1307	CTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGCGTGGGGCTGCAGCGCTACCTCCAG *****
AC012676	82265	CTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGCGTGGGGCTGCAGCGCTACCTCCAG
DNA44804	1367	GGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCGGGCCCTGAT *****
AC012676	82325	GGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCGGGCCCTGAT
DNA44804	1427	AAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTCACCCAGCTG *****
AC012676	82385	AAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTCACCCAGCTG
DNA44804	1487	CGGCCCCAACGCCACTTACTCCGTCTGTGTCATGCCTTTGGGGCCCCGGGCGGGTGCCGGAG *****
AC012676	82445	CGGCCCCAACGCCACTTACTCCGTCTGTGTCATGCCTTTGGGGCCCCGGGCGGGTGCCGGAG
DNA44804	1547	GGCGAGGAGGCCTGCGGGGAGGCCCATACACCCCAGCCGTCCACTCCAACCACGCCCCA *****
AC012676	82505	GGCGAGGAGGCCTGCGGGGAGGCCCATACACCCCAGCCGTCCACTCCAACCACGCCCCA
DNA44804	1607	GTCACCCAGGCCCGCGAGGGCAACCTGCCGCTCCTCATTGCGCCCGCCCTGGCCGCGGTG *****
AC012676	82565	GTCACCCAGGCCCGCGAGGGCAACCTGCCGCTCCTCATTGCGCCCGCCCTGGCCGCGGTG
DNA44804	1667	CTCCTGGCCGCGCTGGCTGCGGTGGGGGCAGCCTACTGTGTGCGGCGGGGCGGGCCATG *****
AC012676	82625	CTCCTGGCCGCGCTGGCTGCGGTGGGGGCAGCCTACTGTGTGCGGCGGGGCGGGCCATG
DNA44804	1727	GCAGCAGCGGCTCAGGACAAAGGGCAGGTGGGGCCAGGGGCTGGGCCCCCTGGAAGTGGAG *****
AC012676	82685	GCAGCAGCGGCTCAGGACAAAGGGCAGGTGGGGCCAGGGGCTGGGCCCCCTGGAAGTGGAG
DNA44804	1787	GGAGTGAAGTCCCCTTGAGCCAGGCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTG *****
AC012676	82745	GGAGTGAAGTCCCCTTGAGCCAGGCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTG
DNA44804	1847	CCCAGCGGGTCTGAGTGTGAGGTGCCACTCATGGGCTTCCCAGGGCCTGGCCTCCAGTCA *****
AC012676	82805	CCCAGCGGGTCTGAGTGTGAGGTGCCACTCATGGGCTTCCCAGGGCCTGGCCTCCAGTCA
DNA44804	1907	CCCCTCACGCAAAGCCCTACATCTAAGCCAGAGAGAGACAGGGCAGCTGGGGCCGGGCT *****
AC012676	82865	CCCCTCACGCAAAGCCCTACATCTAAGCCAGAGAGAGACAGGGCAGCTGGGGCCGGGCT
DNA44804	1967	CTCAGCCAGTGAGATGGCCAGCCCCCTCCTGCTGCCACACCACGTAAGTTCTCAGTCCCA *****
AC012676	82925	CTCAGCCAGTGAGATGGCCAGCCCCCTCCTGCTGCCACACCACGTAAGTTCTCAGTCCCA
DNA44804	2027	ACCTCGGGGATGTGTGCAGACAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGA *****
AC012676	82985	ACCTCGGGGATGTGTGCAGACAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGA
DNA44804	2087	CCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGA *****
AC012676	83045	CCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGA

BLAST RESULTS A-10

DNA44804 2147 ACCGAGTGCCTATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCAC

 AC012676 83105 ACCGAGTGCCTATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCAC

 DNA44804 2207 GGCGGGCCCTGCCATGTGCTGGTAACGCATGCCTGGGCCCTGCTGGGCTCTCCCACTCCA

 AC012676 83165 GGCGGGCCCTGCCATGTGCTGGTAACGCATGCCTGGGCCCTGCTGGGCTCTCCCACTCCA

 DNA44804 2267 GGCGGACCCTGGGGGCCAGTGAAGGAAGCTCCCGGAAAGAGCAGAGGGAGAGCGGGTAGG

 AC012676 83225 GGCGGACCCTGGGGGCCAGTGAAGGAAGCTCCCGGAAAGAGCAGAGGGAGAGCGGGTAGG

 DNA44804 2327 CGGCTGTGTGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAAGAACTGGAAAGGA

 AC012676 83285 CGGCTGTGTGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAAGAACTGGAAAGGA

 DNA44804 2387 AGATGCTTTAGGAACATGTTTTGCTTTTTTAAAATATATATATTTATAAGAGATCCTT

 AC012676 83345 AGATGCTTTAGGAACATGTTTTGCTTTTTTAAAATATATATATTTATAAGAGATCCTT

 DNA44804 2447 TCCCATTTATTCTGGGAAGATGTTTTTCAAACCTCAGAGACAAGGACTTTGGTTTTTGTAA

 AC012676 83405 TCCCATTTATTCTGGGAAGATGTTTTTCAAACCTCAGAGACAAGGACTTTGGTTTTTGTAA

 DNA44804 2507 GACAAACGATGATATGAAGGCCTTTTGTAAAGAAAAATAAAA

 AC012676 83465 GACAAACGATGATATGAAGGCCTTTTGTAAAGAAAAATAAAA

Score = 280 (555 bits), Expect = e-154 [AC012676, seg 2/3]
 Identities = 283/284 (99%), at 127,80860-410,81143, Strand +/+

DNA44804 127 GGGACAGAAGATGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCT

 AC012676 80860 GGGACAGAAGATGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCT

 DNA44804 187 GGGGCCTGGGGTGCAGGGCTGCCATCCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTT

 AC012676 80920 GGGGCCTGGGGTGCAGGGCTGCCATCCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTT

 DNA44804 247 CTGCACTGCCCCGCCAGGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGTGGGGCT

 AC012676 80980 CTGCACTGCCCCGCCAGGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGTGGGGCT

 DNA44804 307 GTACGTCTTTGAGAACGGCATCACCATGCTCGACGCAAGCAGCTTTGCCGGCCTGCCGGG

 AC012676 81040 GTACGTCTTTGAGAACGGCATCACCATGCTCGACGCAAGCAGCTTTGCCGGCCTGCCGGG

 DNA44804 367 CCTGCAGCTCCTGGACCTGTACAGAACCAGATCGCCAGCCTGC

 AC012676 81100 CCTGCAGCTCCTGGACCTGTACAGAACCAGATCGCCAGCCTGC

Score = 128 (254 bits), Expect = 1e-63 [AC012676, seg 3/3]
 Identities = 128/128 (100%), at 1,71859-128,71986, Strand +/-

DNA44804 1 GGGGCGGGTGGACGCGGACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCC

BLAST RESULTS A-19

AC012676 71859 GGGGCGGGTGGACGCGGACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCCCTCGGGCCC

DNA44804 61 GACCCGCCAGGAAAGACTGAGGCCGCGGCCTGCCCCGCCCGGCTCCCTGCGCCGCCGCCG

AC012676 71919 GACCCGCCAGGAAAGACTGAGGCCGCGGCCTGCCCCGCCCGGCTCCCTGCGCCGCCGCCG

DNA44804 121 CCTCCCGG

AC012676 71979 CCTCCCGG

>7 AC005222 Homo sapiens chromosome 16, cosmid clone RT163 (LANL), complete
(40619 bp) [3 segs]
Score = 2138 (4238 bits), Expect = 0.0 [AC005222, seg 1/3]
Identities = 2141/2142 (99%), at 407,22755-2548,24896, Strand +/-

DNA44804 407 CTGCGCCTGCCCCGCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAG

AC005222 22755 CTGCGCCTGCCCCGCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAG

DNA44804 467 CCCGGCATCCTGGACACTGCCAACGTGGAGGCGCTGCGGCTGGCTGGTCTGGGGCTGCAG

AC005222 22815 CCCGGCATCCTGGACACTGCCAACGTGGAGGCGCTGCGGCTGGCTGGTCTGGGGCTGCAG

DNA44804 527 CAGCTGGACGAGGGGCTCTTCAGCCGCTTGCGCAACCTCCACGACCTGGATGTGTCCGAC

AC005222 22875 CAGCTGGACGAGGGGCTCTTCAGCCGCTTGCGCAACCTCCACGACCTGGATGTGTCCGAC

DNA44804 587 AACCAGCTGGAGCGAGTGCCACCTGTGATCCGAGGCCTCCGGGGCCTGACGCGCCTGCGG

AC005222 22935 AACCAGCTGGAGCGAGTGCCACCTGTGATCCGAGGCCTCCGGGGCCTGACGCGCCTGCGG

DNA44804 647 CTGGCCGGCAACACCCGCATTGCCAGCTGCGGCCCGAGGACCTGGCCGGCCTGGCTGCC

AC005222 22995 CTGGCCGGCAACACCCGCATTGCCAGCTGCGGCCCGAGGACCTGGCCGGCCTGGCTGCC

DNA44804 707 CTGCAGGAGCTGGATGTGAGCAACCTAAGCCTGCAGGCCCTGCCTGGCGACCTCTCGGGC

AC005222 23055 CTGCAGGAGCTGGATGTGAGCAACCTAAGCCTGCAGGCCCTGCCTGGCGACCTCTCGGGC

DNA44804 767 CTCTTCCCCCGCCTGCGGCTGCTGGCAGCTGCCCGCAACCCCTTCAACTGCGTGTGCCCC

AC005222 23115 CTCTTCCCCCGCCTGCGGCTGCTGGCAGCTGCCCGCAACCCCTTCAACTGCGTGTGCCCC

DNA44804 827 CTGAGCTGGTTTGGCCCCCTGGGTGCGCGAGAGCCACGTACACTGGCCAGCCCTGAGGAG

AC005222 23175 CTGAGCTGGTTTGGCCCCCTGGGTGCGCGAGAGCCACGTACACTGGCCAGCCCTGAGGAG

DNA44804 887 ACGCGCTGCCACTTCCCGCCCAAGAACGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCC

AC005222 23235 ACGCGCTGCCACTTCCCGCCCAAGAACGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCC

DNA44804 947 GACTTTGGCTGCCCAGCCACCACCACAGCCACAGTGGCCACCACGAGGCCCGTGGTG

AC005222 23295 GACTTTGGCTGCCCAGCCACCACCACAGCCACAGTGGCCACCACGAGGCCCGTGGTG

DNA44804 1007 CGGGAGCCACAGCCTTGTCTTCTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCG

BVAST RESULTS A-20

AC005222 23355 CGGGAGCCCACAGCCTTGTCTTCTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGAGCCG

DNA44804 1067 GCCACTGAGGCCCCCAGCCCGCCCTCCACTGCCCCACCGACTGTAGGGCCTGTCCCCCAG

AC005222 23415 GCCACTGAGGCCCCCAGCCCGCCCTCCACTGCCCCACCGACTGTAGGGCCTGTCCCCCAG

DNA44804 1127 CCCCAGGACTGCCCACCGTCCACCTGCCTCAATGGGGGCACATGCCACCTGGGGACACGG

AC005222 23475 CCCCAGGACTGCCCACCGTCCACCTGCCTCAATGGGGGCACATGCCACCTGGGGACACGG

DNA44804 1187 CACCACCTGGCGTGCTTGTGCCCCGAAGGCTTCACGGGCCTGTACTGTGAGAGCCAGATG

AC005222 23535 CACCACCTGGCGTGCTTGTGCCCCGAAGGCTTCACGGGCCTGTACTGTGAGAGCCAGATG

DNA44804 1247 GGGCAGGGGACACGGCCAGCCCTACACCAGTCACGCCGAGGCCACCACGGTCCCTGACC

AC005222 23595 GGGCAGGGGACACGGCCAGCCCTACACCAGTCACGCCGAGGCCACCACGGTCCCTGACC

DNA44804 1307 CTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGCGTGGGGCTGCAGCGCTACCTCCAG

AC005222 23655 CTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGCGTGGGGCTGCAGCGCTACCTCCAG

DNA44804 1367 GGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCGGGCCCTGAT

AC005222 23715 GGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCGGGCCCTGAT

DNA44804 1427 AAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTCACCCAGCTG

AC005222 23775 AAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTCACCCAGCTG

DNA44804 1487 CGGCCCAACGCCACTTACTCCGTCTGTGTCATGCCTTTGGGGCCCGGGCGGGTGCCGGAG

AC005222 23835 CGGCCCAACGCCACTTACTCCGTCTGTGTCATGCCTTTGGGGCCCGGGCGGGTGCCGGAG

DNA44804 1547 GGCGAGGAGGCCTGCGGGGAGGCCCATACACCCCAGCCGTCCACTCCAACCACGCCCCA

AC005222 23895 GGCGAGGAGGCCTGCGGGGAGGCCCATACACCCCAGCCGTCCACTCCAACCACGCCCCA

DNA44804 1607 GTCACCCAGGCCCGCGAGGGCAACCTGCCGCTCCTCATTGCGCCCGCCCTGGCCGCGGTG

AC005222 23955 GTCACCCAGGCCCGCGAGGGCAACCTGCCGCTCCTCATTGCGCCCGCCCTGGCCGCGGTG

DNA44804 1667 CTCCTGGCCGCGCTGGCTGCGGTGGGGGCAGCCTACTGTGTGCGGCGGGGGCGGGCCATG

AC005222 24015 CTCCTGGCCGCGCTGGCTGCGGTGGGGGCAGCCTACTGTGTGCGGCGGGGGCGGGCCATG

DNA44804 1727 GCAGCAGCGGCTCAGGACAAAGGGCAGGTGGGGCCAGGGGCTGGGCCCCTGGAACCTGGAG

AC005222 24075 GCAGCAGCGGCTCAGGACAAAGGGCAGGTGGGGCCAGGGGCTGGGCCCCTGGAACCTGGAG

DNA44804 1787 GGAGTGAAGGTCCCCTTGAGCCAGGCCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTG

AC005222 24135 GGAGTGAAGGTCCCCTTGAGCCAGGCCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTG

DNA44804 1847 CCCAGCGGGTCTGAGTGTGAGGTGCCACTCATGGGCTTCCCAGGGCCTGGCCTCCAGTCA

AC005222 24195 CCCAGCGGGTCTGAGTGTGAGGTGCCACTCATGGGCTTCCCAGGGCCTGGCCTCCAGTCA

BLAST RESULTS A-21

DNA44804 1907 CCCCTCCACGCAAAGCCCTACATCTAAGCCAGAGAGAGACAGGGCAGCTGGGGCCGGGCT

 AC005222 24255 CCCCTCCACGCAAAGCCCTACATCTAAGCCAGAGAGAGACAGGGCAGCTGGGGCCGGGCT

 DNA44804 1967 CTCAGCCAGTGAGATGGCCAGCCCCCTCTGCTGCCACACCACGTAAGTTCTCAGTCCCA

 AC005222 24315 CTCAGCCAGTGAGATGGCCAGCCCCCTCTGCTGCCACACCACGTAAGTTCTCAGTCCCA

 DNA44804 2027 ACCTCGGGGATGTGTGCAGACAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGA

 AC005222 24375 ACCTCGGGGATGTGTGCAGACAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGA

 DNA44804 2087 CCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCCAGCTGACGAGCCCTAACGTCCCCAGA

 AC005222 24435 CCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCCAGCTGACGAGCCCTAACGTCCCCAGA

 DNA44804 2147 ACCGAGTGCCTATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCAC

 AC005222 24495 ACCGAGTGCCTATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCAC

 DNA44804 2207 GGCGGGCCCTGCCATGTGCTGGTAACGCATGCCTGGGCCCTGCTGGGCTCTCCCACTCCA

 AC005222 24555 GGCGGGCCCTGCCATGTGCTGGTAACGCATGCCTGGGCCCTGCTGGGCTCTCCCACTCCA

 DNA44804 2267 GGCGGACCCTGGGGGCCAGTGAAGGAAGCTCCCGGAAAGAGCAGAGGGAGAGCGGGTAGG

 AC005222 24615 GGCGGACCCTGGGGGCCAGTGAAGGAAGCTCCCGGAAAGAGCAGAGGGAGAGCGGGTAGG

 DNA44804 2327 CGGCTGTGTGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAAGAACTGGAAAGGA

 AC005222 24675 CGGCTGTGTGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAAGAACTGGAAAGGA

 DNA44804 2387 AGATGCTTTAGGAACATGTTTTGCTTTTTTAAATATATATATATTATAAGAGATCCTT

 AC005222 24735 AGATGCTTTAGGAACATGTTTTGCTTTTTTAAATATATATATATTATAAGAGATCCTT

 DNA44804 2447 TCCCATTATTTCTGGGAAGATGTTTTCAAACCTCAGAGACAAGGACTTTGGTTTTTTGTAA

 AC005222 24795 TCCCATTATTTCTGGGAAGATGTTTTCAAACCTCAGAGACAAGGACTTTGGTTTTTTGTAA

 DNA44804 2507 GACAAACGATGATATGAAGGCCTTTTGTAGAAAAAATAAAA

 AC005222 24855 GACAAACGATGATATGAAGGCCTTTTGTAGAAAAAATAAAA

Score = 280 (555 bits), Expect = e-154 [AC005222, seg 2/3]
 Identities = 283/284 (99%), at 127,22250-410,22533, Strand +/-

DNA44804 127 GGGACAGAAGATGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCT

 AC005222 22250 GGGACAGAAGATGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCT

 DNA44804 187 GGGGCCTGGGGTGCAGGGCTGCCATCCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTT

 AC005222 22310 GGGGCCTGGGGTGCAGGGCTGCCATCCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTT

 DNA44804 247 CTGCACTGCCCCCAGGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGTGGGGCT

BLAST RESULTS A-22

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*****
AC005222 22370 CTGCACTGCCCCGCCAGGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGTGGGGCT
DNA44804 307 GTACGTCTTTGAGAACGGCATCACCATGCTCGACGCAAGCAGCTTTGCCGGCCTGCCGGG
*****
AC005222 22430 GTACGTCTTTGAGAACGGCATCACCATGCTCGACGCAAGCAGCTTTGCCGGCCTGCCGGG
DNA44804 367 CCTGCAGTCCTGGACCTGTCACAGAACCAGATCGCCAGCCTGC
*****
AC005222 22490 CCTGCAGTCCTGGACCTGTCACAGAACCAGATCGCCAGCCTGC

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Score = 128 (254 bits), Expect = 1e-63 [AC005222, seg 3/3]
Identities = 128/128 (100%), at 1,13249-128,13376, Strand +/+

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DNA44804 1 GGGGCGGGTGGACGCGGACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCCCTCGGGCCC
*****
AC005222 13249 GGGGCGGGTGGACGCGGACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCCCTCGGGCCC
DNA44804 61 GACCCGCCAGGAAAGACTGAGGCCGCGGCCTGCCCCGCCCGGCTCCCTGCGCCGCCGCCG
*****
AC005222 13309 GACCCGCCAGGAAAGACTGAGGCCGCGGCCTGCCCCGCCCGGCTCCCTGCGCCGCCGCCG
DNA44804 121 CCTCCCGG
*****
AC005222 13369 CCTCCCGG

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>8 P_AAF44105 Human PRO1282 (UNQ652) nucleotide sequence SEQ ID NO:51. (2768 bp)
[2 segs]

Score = 2127 (4216 bits), Expect = 0.0 [P_AAF44105, seg 1/2]
Identities = 2139/2142 (99%), Gaps = 2/2142 (0%), at 407,615-2548,2754, Strand +/+

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DNA44804 407 CTGCGCCTGCCCCGCCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAG
*****
P_AAF44105 615 CTGCGCCTGCCCCGCCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAG
DNA44804 467 CCCGGCATCCTGGACACTGCCAACGTGGAGGCGCTGCGGCTGGCTGGTCTGGGGCTGCAG
*****
P_AAF44105 675 CCCGGCATCCTGGACACTGCCAACGTGGAGGCGCTGCGGCTGGCTGGTCTGGGGCTGCAG
DNA44804 527 CAGCTGGACGAGGGGCTCTTCAGCCGCTTGCGCAACCTCCACGACCTGGATGTGTCCGAC
*****
P_AAF44105 735 CAGCTGGACGAGGGGCTCTTCAGCCGCTTGCGCAACCTCCACGACCTGGATGTGTCCGAC
DNA44804 587 AACCAGCTGGAGCGAGTGCCACCTGTGATCCGAGGCCTCCGGGGCCTGACGCGCCTGCGG
*****
P_AAF44105 795 AACCAGCTGGAGCGAGTGCCACCTGTGATCCGAGGCCTCCGGGGCCTGACGCGCCTGCGG
DNA44804 647 CTGGCCGGCAACACCCGCATTGCCCAGCTGCGGCCCGAGGACCTGGCCGGCCTGGCTGCC
*****
P_AAF44105 855 CTGGCCGGCAACACCCGCATTGCCCAGCTGCGGCCCGAGGACCTGGCCGGCCTGGCTGCC
DNA44804 707 CTGCAGGAGCTGGATGTGAGCAACCTAAGCCTGCAGGCCCTGCCTGGCGACCTCTCGGGC
*****
P_AAF44105 915 CTGCAGGAGCTGGATGTGAGCAACCTAAGCCTGCAGGCCCTGCCTGGCGACCTCTCGGGC
DNA44804 767 CTCTTCCCCCGCCTGCGGCTGCTGGCAGCTGCCCCGAACCCCTTCAACTGCGTGTGCCCC

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BLAST RESULTS A-23

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*****
P_AAF44105 975 CTCTTCCCCCGCCTGCGGCTGCTGGCAGCTGCCCGAACCCCTTCAACTGCGTGTGCCCC
DNA44804 827 CTGAGCTGGTTTGGCCCCCTGGGTGCGCGAGAGCCACGTCACACTGGCCAGCCCTGAGGAG
*****
P_AAF44105 1035 CTGAGCTGGTTTGGCCCCCTGGGTGCGCGAGAGCCACGTCACACTGGCCAGCCCTGAGGAG
DNA44804 887 ACGCGCTGCCACTTCCCGCCCAAGAACGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCC
*****
P_AAF44105 1095 ACGCGCTGCCACTTCCCGCCCAAGAACGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCC
DNA44804 947 GACTTTGGCTGCCCAGCCACCACCACAGCCACAGTGCCCACCACGAGGCCCGTGGTG
*****
P_AAF44105 1155 GACTTTGGCTGCCCAGCCACCACCACAGCCACAGTGCCCACCACGAGGCCCGTGGTG
DNA44804 1007 CGGGAGCCACAGCCTTGCTTCTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGCGCG
*****
P_AAF44105 1215 CGGGAGCCACAGCCTTGCTTCTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGCGCG
DNA44804 1067 GCCACTGAGGCCCCAGCCCGCCTCCACTGCCCCACCGACTGTAGGGCCTGTCCCCAG
*****
P_AAF44105 1275 GCCACTGAGGCCCCAGCCCGCCTCCACTGCCCCACCGACTGTAGGGCCTGTCCCCAG
DNA44804 1127 CCCCAGGACTGCCACCGTCCACCTGCCTCAATGGGGGCACATGCCACCTGGGGACACGG
*****
P_AAF44105 1335 CCCCAGGACTGCCACCGTCCACCTGCCTCAATGGGGGCACATGCCACCTGGGGACACGG
DNA44804 1187 CACCACCTGGCGTGCTTGTGCCCCGAAGGCTTCACGGGCCTGTACTGTGAGAGCCAGATG
*****
P_AAF44105 1395 CACCACCTGGCGTGCTTGTGCCCCGAAGGCTTCACGGGCCTGTACTGTGAGAGCCAGATG
DNA44804 1247 GGGCAGGGGACACGGCCAGCCCTACACCAGTCACGCCGAGGCCACCACGGTCCCTGACC
*****
P_AAF44105 1455 GGGCAGGGGACACGGCCAGCCCTACACCAGTCACGCCGAGGCCACCACGGTCCCTGACC
DNA44804 1307 CTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGCGTGGGGCTGCAGCGCTACCTCCAG
*****
P_AAF44105 1515 CTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGCGTGGGGCTGCAGCGCTACCTCCAG
DNA44804 1367 GGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCGGGCCCTGAT
*****
P_AAF44105 1575 GGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCGGGCCCTGAT
DNA44804 1427 AAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTCACCCAGCTG
*****
P_AAF44105 1635 AAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTCACCCAGCTG
DNA44804 1487 CGGCCCCAACGCCACTTACTCCGTCTGTGTCATGCCTTTGGGGCCCGGGCGGGTGCCGGAG
*****
P_AAF44105 1695 CGGCCCCAACGCCACTTACTCCGTCTGTGTCATGCCTTTGGGGCCCGGGCGGGTGCCGGAG
DNA44804 1547 GGCGAGGAGGCCTGCGGGGAGGCCCATACACCCAGCCGTCCACTCCAACCACGCCCCA
*****
P_AAF44105 1755 GGCGAGGAGGCCTGCGGGGAGGCCCATACACCCAGCCGTCCACTCCAACCACGCCCCA
DNA44804 1607 GTCACCCAGGCCCGCGAGGGCAACCTGCCGCTCCTCATTGCGCCCGCCCTGGCCGCGGTG
*****

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BLAST RESULTS A-24

P_AAF44105 1815 GTCACCCAGGCCCGCGAGGGCAACCTGCCGCTCCTCATTGCGCCCGCCCTGGCCGCGGTG

DNA44804 1667 CTCCTGGCCGCGCTGGCTGCGGTGGGGGCAGCCTACTGTGTGCGGCGGGGCGGGCCATG

P_AAF44105 1875 CTCCTGGCCGCGCTGGCTGCGGTGGGGGCAGCCTACTGTGTGCGGCGGGGCGGGCCATG

DNA44804 1727 GCAGCAGCGGCTCAGGACAAAGGGCAGGTGGGGCCAGGGGCTGGGCCCTGGAAGTGGAG

P_AAF44105 1935 GCAGCAGCGGCTCAGGACAAAGGGCAGGTGGGGCCAGGGGCTGGGCCCTGGAAGTGGAG

DNA44804 1787 GGAGTGAAGGTCCCCTTGGAGCCAGGCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTG

P_AAF44105 1995 GGAGTGAAGGTCCCCTTGGAGCCAGGCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTG

DNA44804 1847 CCCAGCGGGTCTGAGTGTGAGGTGCCACTCATGGGCTTCCAGGGCTGGCCTCCAGTCA

P_AAF44105 2055 CCCAGCGGGTCTGAGTGTGAGGTGCCACTCATGGGCTTCCAGGGCTGGCCTCCAGTCA

DNA44804 1907 CCCCTCCACGCAAAGCCCTACATCTAAGCCAGAGAGAGACAGGGCAGCTGGGGCCGGGCT

P_AAF44105 2115 CCCCTCCACGCAAAGCCCTACATCTAAGCCAGAGAGAGACAGGGCAGCTGGGGCCGGGCT

DNA44804 1967 CTCAGCCAGTGAGATGGCCAGCCCCCTCCTGCTGCCACACCACGTAAGTTCTCAGTCCCA

P_AAF44105 2175 CTCAGCCAGTGAGATGGCCAGCCCCCTCCTGCTGCCACACCACGTAAGTTCTCAGTCCCA

DNA44804 2027 ACCTCGGGGATGTGTGCAGACAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGA

P_AAF44105 2235 ACCTCGGGGATGTGTGCAGACAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGA

DNA44804 2087 CCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCCAGCTGACGAGCCCTAACGTCCCCAGA

P_AAF44105 2295 CCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCCAGCTGACGAGCCCTAACGTCCCCAGA

DNA44804 2147 ACCGAGTGCCTATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCAC

P_AAF44105 2355 ACCGAGTGCCTATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCAC

DNA44804 2207 GGCGGGCCCTGCCATGTGCTGGTAACGCATGCCTGGGCCCTGCTGGGCTCTCCCACTCCA

P_AAF44105 2415 GGCGGGCCCTGCCATGTGCTGGTAACGCATGCCTGGGTCCTGCTGGGCTCTCCCACTCCA

DNA44804 2267 GGCGGACCCTGGGGGCCAGTGAAGGAAGCTCCCGAAAGAGCAGAGGGAGAGCGGGTAGG

P_AAF44105 2475 GGCGGACCCTGGGGGCCAGTGAAGGAAGCTCCCGAAAGAGCAGAGGGAGAGCGGGTAGG

DNA44804 2327 CGGCTGTGTGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAAGAACTGGAAGGA

P_AAF44105 2535 CGGCTGTGTGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAAGAACTGGAAGGA

DNA44804 2387 AGATGCTTTAGGAACATGTTTTGCTTTTTTAAATATATATATTTATAAGAGATCCTT

P_AAF44105 2595 AGATGCTTTAGGAACATGTTTTGCTTTTTTAAA--ATATATATATTTATAAGAGATCCTT

DNA44804 2447 TCCCATTTATTCTGGGAAGATGTTTTTCAAACCTCAGAGACAAGGACTTTGGTTTTTGTAA

P_AAF44105 2653 TCCCATTTATTCTGGGAAGATGTTTTTCAAACCTCAGAGACAAGGACTTTGGTTTTTGTAA

Blast Results A-25

DNA44804 2507 GACAAACGATGATATGAAGGCCTTTTGTAGAAAAAATAAAA

 P_AAF44105 2713 GACAAACGATGATATGAAGGCCTTTTGTAGAAAAAATAAAA

Score = 389 (771 bits), Expect = 0.0 [P_AAF44105, seg 2/2]
 Identities = 392/393 (99%), at 18,1-410,393, Strand +/+

DNA44804 18 ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCCTCGGGCCCGACCCGCCAGGAAAGAC

 P_AAF44105 1 ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCCTCGGGCCCGACCCGCCAGGAAAGAC

DNA44804 78 TGAGGCCGCGGCCTGCCCCGCCGGCTCCCTGCGCCCGCCGCTCCCGGGACAGAAGA

 P_AAF44105 61 TGAGGCCGCGGCCTGCCCCGCCGGCTCCCTGCGCCCGCCGCTCCCGGGACAGAAGA

DNA44804 138 TGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCTGGGGCCTGGGG

 P_AAF44105 121 TGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCTGGGGCCTGGGG

DNA44804 198 TGCAGGGCTGCCCATCCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTTCTGCACTGCCC

 P_AAF44105 181 TGCAGGGCTGCCCATCCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTTCTGCACTGCCC

DNA44804 258 GCCAGGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGTGGGGCTGTACGTCTTTG

 P_AAF44105 241 GCCAGGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGTGGGGCTGTACGTCTTTG

DNA44804 318 AGAACGGCATCACCATGCTCGACGCAAGCAGCTTTGCCGGCCTGCCGGGCCTGCAGCTCC

 P_AAF44105 301 AGAACGGCATCACCATGCTCGACGCAAGCAGCTTTGCCGGCCTGCCGGGCCTGCAGCTCC

DNA44804 378 TGGACCTGTCACAGAACCAGATCGCCAGCCTGC

 P_AAF44105 361 TGGACCTGTCACAGAACCAGATCGCCAGCCTGC

>9 P_AAF92065 Human PRO1282 cDNA. (2768 bp) [2 segs]
 Score = 2127 (4216 bits), Expect = 0.0 [P_AAF92065, seg 1/2]
 Identities = 2139/2142 (99%), Gaps = 2/2142 (0%), at 407,615-2548,2754, Strand
 +/+

DNA44804 407 CTGCGCCTGCCCCGCCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAG

 P_AAF92065 615 CTGCGCCTGCCCCGCCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAG

DNA44804 467 CCCGGCATCCTGGACACTGCCAACGTGGAGGCGCTGCGGCTGGCTGGTCTGGGGCTGCAG

 P_AAF92065 675 CCCGGCATCCTGGACACTGCCAACGTGGAGGCGCTGCGGCTGGCTGGTCTGGGGCTGCAG

DNA44804 527 CAGCTGGACGAGGGGCTCTTCAGCCGCTTGCGCAACCTCCACGACCTGGATGTGTCCGAC

 P_AAF92065 735 CAGCTGGACGAGGGGCTCTTCAGCCGCTTGCGCAACCTCCACGACCTGGATGTGTCCGAC

DNA44804 587 AACCAGCTGGAGCGAGTGCCACCTGTGATCCGAGGCCTCCGGGGCCTGACGCGCCTGCGG

 P_AAF92065 795 AACCAGCTGGAGCGAGTGCCACCTGTGATCCGAGGCCTCCGGGGCCTGACGCGCCTGCGG

BLAST RESULTS A-26

DNA44804	647	CTGGCCGGCAACACCCGCATTGCCAGCTGCGGCCCCGAGGACCTGGCCGGCCTGGCTGCC

P_AAF92065	855	CTGGCCGGCAACACCCGCATTGCCAGCTGCGGCCCCGAGGACCTGGCCGGCCTGGCTGCC
DNA44804	707	CTGCAGGAGCTGGATGTGAGCAACCTAAGCCTGCAGGCCCTGCCTGGCGACCTCTCGGGC

P_AAF92065	915	CTGCAGGAGCTGGATGTGAGCAACCTAAGCCTGCAGGCCCTGCCTGGCGACCTCTCGGGC
DNA44804	767	CTCTTCCCCCGCCTGCGGCTGCTGGCAGCTGCCCCGAACCCCTTCAACTGCGTGTGCCCC

P_AAF92065	975	CTCTTCCCCCGCCTGCGGCTGCTGGCAGCTGCCCCGAACCCCTTCAACTGCGTGTGCCCC
DNA44804	827	CTGAGCTGGTTTGGCCCTGGGTGCGCGAGAGCCACGTCACTGGCCAGCCCTGAGGAG

P_AAF92065	1035	CTGAGCTGGTTTGGCCCTGGGTGCGCGAGAGCCACGTCACTGGCCAGCCCTGAGGAG
DNA44804	887	ACGCGCTGCCACTTCCCGCCCAAGAACGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCC

P_AAF92065	1095	ACGCGCTGCCACTTCCCGCCCAAGAACGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCC
DNA44804	947	GACTTTGGCTGCCCAGCCACCACCACACAGCCACAGTGCCCACCACGAGGCCCGTGGTG

P_AAF92065	1155	GACTTTGGCTGCCCAGCCACCACCACACAGCCACAGTGCCCACCACGAGGCCCGTGGTG
DNA44804	1007	CGGGAGCCCACAGCCTTGCTCTTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCG

P_AAF92065	1215	CGGGAGCCCACAGCCTTGCTCTTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCG
DNA44804	1067	GCCACTGAGGCCCCAGCCCGCCCTCCACTGCCCCACCGACTGTAGGGCCTGTCCCCCAG

P_AAF92065	1275	GCCACTGAGGCCCCAGCCCGCCCTCCACTGCCCCACCGACTGTAGGGCCTGTCCCCCAG
DNA44804	1127	CCCCAGGACTGCCACCGTCCACCTGCCTCAATGGGGGCACATGCCACCTGGGGACACGG

P_AAF92065	1335	CCCCAGGACTGCCACCGTCCACCTGCCTCAATGGGGGCACATGCCACCTGGGGACACGG
DNA44804	1187	CACCACCTGGCGTGCTTGTGCCCCGAAGGCTTCACGGGCCTGTACTGTGAGAGCCAGATG

P_AAF92065	1395	CACCACCTGGCGTGCTTGTGCCCCGAAGGCTTCACGGGCCTGTACTGTGAGAGCCAGATG
DNA44804	1247	GGGCAGGGGACACGGCCAGCCCTACACAGTCACGCCGAGGCCACCACGGTCCCTGACC

P_AAF92065	1455	GGGCAGGGGACACGGCCAGCCCTACACAGTCACGCCGAGGCCACCACGGTCCCTGACC
DNA44804	1307	CTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGCGTGGGGCTGCAGCGCTACCTCCAG

P_AAF92065	1515	CTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGCGTGGGGCTGCAGCGCTACCTCCAG
DNA44804	1367	GGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCGGGCCCTGAT

P_AAF92065	1575	GGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCGGGCCCTGAT
DNA44804	1427	AAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTCACCCAGCTG

P_AAF92065	1635	AAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTCACCCAGCTG
DNA44804	1487	CGGCCCAACGCCACTTACTCCGTCTGTGTCATGCCTTTGGGGCCCGGGCGGGTGCCGGAG

BLAST RESULTS A-27

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*****
P_AAF92065 1695 CGGCCCAACGCCACTTACTCCGTCTGTGTCATGCCTTTGGGGCCCCGGGCGGGTGCCGGAG
DNA44804 1547 GCGGAGGAGGCCTGCGGGGAGGCCCATACACCCCAGCCGTCCACTCCAACCACGCCCCA
*****
P_AAF92065 1755 GCGGAGGAGGCCTGCGGGGAGGCCCATACACCCCAGCCGTCCACTCCAACCACGCCCCA
DNA44804 1607 GTCACCCAGGCCCGCGGAGGGCAACCTGCCGCTCCTCATTGCGCCCGCCCTGGCCGCGGTG
*****
P_AAF92065 1815 GTCACCCAGGCCCGCGGAGGGCAACCTGCCGCTCCTCATTGCGCCCGCCCTGGCCGCGGTG
DNA44804 1667 CTCCTGGCCGCGCTGGCTGCGGTGGGGGCAGCCTACTGTGTGCGGCGGGGCGGGCCATG
*****
P_AAF92065 1875 CTCCTGGCCGCGCTGGCTGCGGTGGGGGCAGCCTACTGTGTGCGGCGGGGCGGGCCATG
DNA44804 1727 GCAGCAGCGGCTCAGGACAAAGGGCAGGTGGGGCCAGGGGCTGGGCCCCCTGGAAGTGGAG
*****
P_AAF92065 1935 GCAGCAGCGGCTCAGGACAAAGGGCAGGTGGGGCCAGGGGCTGGGCCCCCTGGAAGTGGAG
DNA44804 1787 GGAGTGAAGGTCCCCTTGGAGCCAGGCCCAAGGCAACAGAGGGCGGTGGAGAGGCCCTG
*****
P_AAF92065 1995 GGAGTGAAGGTCCCCTTGGAGCCAGGCCCAAGGCAACAGAGGGCGGTGGAGAGGCCCTG
DNA44804 1847 CCCAGCGGGTCTGAGTGTGAGGTGCCACTCATGGGCTTCCCAGGGCCTGGCCTCCAGTCA
*****
P_AAF92065 2055 CCCAGCGGGTCTGAGTGTGAGGTGCCACTCATGGGCTTCCCAGGGCCTGGCCTCCAGTCA
DNA44804 1907 CCCCTCCACGCAAAGCCCTACATCTAAGCCAGAGAGACAGGGCAGCTGGGGCCGGGCT
*****
P_AAF92065 2115 CCCCTCCACGCAAAGCCCTACATCTAAGCCAGAGAGACAGGGCAGCTGGGGCCGGGCT
DNA44804 1967 CTCAGCCAGTGAGATGGCCAGCCCCCTCCTGCTGCCACACCACGTAAGTTCTCAGTCCCA
*****
P_AAF92065 2175 CTCAGCCAGTGAGATGGCCAGCCCCCTCCTGCTGCCACACCACGTAAGTTCTCAGTCCCA
DNA44804 2027 ACCTCGGGGATGTGTGCAGACAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCTCTGGA
*****
P_AAF92065 2235 ACCTCGGGGATGTGTGCAGACAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCTCTGGA
DNA44804 2087 CCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGA
*****
P_AAF92065 2295 CCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGA
DNA44804 2147 ACCGAGTGCCTATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCAC
*****
P_AAF92065 2355 ACCGAGTGCCTATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCAC
DNA44804 2207 GGCGGGCCCTGCCATGTGCTGGTAACGCATGCCTGGGCCCTGCTGGGCTCTCCCACTCCA
*****
P_AAF92065 2415 GGCGGGCCCTGCCATGTGCTGGTAACGCATGCCTGGGTCTGCTGGGCTCTCCCACTCCA
DNA44804 2267 GGCGGACCTGGGGGCCAGTGAAGGAAGCTCCCGAAAGAGCAGAGGGAGAGCGGGTAGG
*****
P_AAF92065 2475 GGCGGACCTGGGGGCCAGTGAAGGAAGCTCCCGAAAGAGCAGAGGGAGAGCGGGTAGG
DNA44804 2327 CGGCTGTGTGACTCTAGTCTTGCCCCAGGAAGCGAAGGAACAAAAGAACTGGAAAGGA
*****

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BLAST RESULTS A-28

P_AAF92065 2535 CGGCTGTGTGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAAGAACTGGAAAGGA
 DNA44804 2387 AGATGCTTTAGGAACATGTTTTGCTTTTTTAAATATATATATATTTATAAGAGATCCTT

 P_AAF92065 2595 AGATGCTTTAGGAACATGTTTTGCTTTTTTAAA--ATATATATATTTATAAGAGATCCTT
 DNA44804 2447 TCCCATTTATTCTGGGAAGATGTTTTCAAACCTCAGAGACAAGGACTTTGGTTTTTGTA

 P_AAF92065 2653 TCCCATTTATTCTGGGAAGATGTTTTCAAACCTCAGAGACAAGGACTTTGGTTTTTGTA
 DNA44804 2507 GACAAACGATGATATGAAGGCCTTTTGTAAGAAAAATAAAA

 P_AAF92065 2713 GACAAACGATGATATGAAGGCCTTTTGTAAGAAAAATAAAA

Score = 389 (771 bits), Expect = 0.0 [P_AAF92065, seg 2/2]
 Identities = 392/393 (99%), at 18,1-410,393, Strand +/+

DNA44804 18 ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCGACCCGCCAGGAAAGAC

 P_AAF92065 1 ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCGACCCGCCAGGAAAGAC
 DNA44804 78 TGAGGCCGCGGCCTGCCCCGCGCGCTCCCTGCGCGCCGCGCCTCCCGGGACAGAAGA

 P_AAF92065 61 TGAGGCCGCGGCCTGCCCCGCGCGCTCCCTGCGCGCCGCGCCTCCCGGGACAGAAGA
 DNA44804 138 TGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCTGGGGCCTGGGG

 P_AAF92065 121 TGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCTGGGGCCTGGGG
 DNA44804 198 TGCAGGGCTGCCCATCCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTTCTGCACTGCC

 P_AAF92065 181 TGCAGGGCTGCCCATCCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTTCTGCACTGCC
 DNA44804 258 GCCAGGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGTGGGGCTGTACGTCTTG

 P_AAF92065 241 GCCAGGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGTGGGGCTGTACGTCTTG
 DNA44804 318 AGAACGGCATCACCATGCTCGACGCAAGCAGCTTTGCCGGCCTGCCGGGCCTGCAGCTCC

 P_AAF92065 301 AGAACGGCATCACCATGCTCGACGCAAGCAGCTTTGCCGGCCTGCCGGGCCTGCAGCTCC
 DNA44804 378 TGGACCTGTCACAGAACCAGATCGCCAGCCTGC

 P_AAF92065 361 TGGACCTGTCACAGAACCAGATCGCCAGCCTGC

>10 P_AA264959 Membrane-bound protein PRO1282 encoding cDNA. (2768 bp) [2 segs]
 Score = 2127 (4216 bits), Expect = 0.0 [P_AA264959, seg 1/2]
 Identities = 2139/2142 (99%), Gaps = 2/2142 (0%), at 407,615-2548,2754, Strand
 +/+

DNA44804 407 CTGCGCCTGCCCCGCCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAG

 P_AA264959 615 CTGCGCCTGCCCCGCCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAG
 DNA44804 467 CCCGGCATCCTGGACACTGCCAACGTGGAGGCGCTGCGGCTGGCTGGTCTGGGGCTGCAG

 P_AA264959 675 CCCGGCATCCTGGACACTGCCAACGTGGAGGCGCTGCGGCTGGCTGGTCTGGGGCTGCAG

BLAST RESULTS A-29

DNA44804	527	CAGCTGGACGAGGGGCTCTTCAGCCGCTTGCGCAACCTCCACGACCTGGATGTGTCCGAC

P_AA264959	735	CAGCTGGACGAGGGGCTCTTCAGCCGCTTGCGCAACCTCCACGACCTGGATGTGTCCGAC
DNA44804	587	AACCAGCTGGAGCGAGTGCCACCTGTGATCCGAGGCCTCCGGGGCCTGACGCGCCTGCGG

P_AA264959	795	AACCAGCTGGAGCGAGTGCCACCTGTGATCCGAGGCCTCCGGGGCCTGACGCGCCTGCGG
DNA44804	647	CTGGCCGGCAACACCCGCATTGCCAGCTGCGGCCGAGGACCTGGCCGGCCTGGCTGCC

P_AA264959	855	CTGGCCGGCAACACCCGCATTGCCAGCTGCGGCCGAGGACCTGGCCGGCCTGGCTGCC
DNA44804	707	CTGCAGGAGCTGGATGTGAGCAACCTAAGCCTGCAGGCCCTGCCTGGCGACCTCTCGGGC

P_AA264959	915	CTGCAGGAGCTGGATGTGAGCAACCTAAGCCTGCAGGCCCTGCCTGGCGACCTCTCGGGC
DNA44804	767	CTCTTCCCCCGCCTGCGGCTGCTGGCAGCTGCCCCGAACCCCTTCAACTGCGTGTGCCCC

P_AA264959	975	CTCTTCCCCCGCCTGCGGCTGCTGGCAGCTGCCCCGAACCCCTTCAACTGCGTGTGCCCC
DNA44804	827	CTGAGCTGGTTTGGCCCCCTGGGTGCGGAGAGCCACGTACACTGGCCAGCCCTGAGGAG

P_AA264959	1035	CTGAGCTGGTTTGGCCCCCTGGGTGCGGAGAGCCACGTACACTGGCCAGCCCTGAGGAG
DNA44804	887	ACGCGCTGCCACTTCCCCGCCAAGAACGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCC

P_AA264959	1095	ACGCGCTGCCACTTCCCCGCCAAGAACGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCC
DNA44804	947	GACTTTGGCTGCCAGCCACCACCACACAGCCACAGTGCCACCACGAGGCCCGTGGTG

P_AA264959	1155	GACTTTGGCTGCCAGCCACCACCACACAGCCACAGTGCCACCACGAGGCCCGTGGTG
DNA44804	1007	CGGGAGCCACAGCCTTGCTCTTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCG

P_AA264959	1215	CGGGAGCCACAGCCTTGCTCTTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCG
DNA44804	1067	GCCACTGAGGCCCCAGCCCGCCTCCACTGCCCCACCGACTGTAGGGCCTGTCCCCAG

P_AA264959	1275	GCCACTGAGGCCCCAGCCCGCCTCCACTGCCCCACCGACTGTAGGGCCTGTCCCCAG
DNA44804	1127	CCCCAGGACTGCCACCGTCCACCTGCCTCAATGGGGGCACATGCCACCTGGGGACACGG

P_AA264959	1335	CCCCAGGACTGCCACCGTCCACCTGCCTCAATGGGGGCACATGCCACCTGGGGACACGG
DNA44804	1187	CACCACCTGGCGTGCTTGTGCCCCGAAGGCTTCACGGGCCTGTACTGTGAGAGCCAGATG

P_AA264959	1395	CACCACCTGGCGTGCTTGTGCCCCGAAGGCTTCACGGGCCTGTACTGTGAGAGCCAGATG
DNA44804	1247	GGGCAGGGGACACGGCCAGCCCTACACCAGTCACGCCGAGGCCACCACGGTCCCTGACC

P_AA264959	1455	GGGCAGGGGACACGGCCAGCCCTACACCAGTCACGCCGAGGCCACCACGGTCCCTGACC
DNA44804	1307	CTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGCGTGGGGCTGCAGCGCTACCTCCAG

P_AA264959	1515	CTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGCGTGGGGCTGCAGCGCTACCTCCAG

BLAST RESULTS A-30

DNA44804	1367	GGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCGGGCCCTGAT

P_AA264959	1575	GGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCGGGCCCTGAT
DNA44804	1427	AAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTCACCCAGCTG

P_AA264959	1635	AAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTCACCCAGCTG
DNA44804	1487	CGGCCCAACGCCACTTACTCCGTCTGTGTCATGCCTTTGGGGCCCCGGGCGGGTGCCGGAG

P_AA264959	1695	CGGCCCAACGCCACTTACTCCGTCTGTGTCATGCCTTTGGGGCCCCGGGCGGGTGCCGGAG
DNA44804	1547	GGCGAGGAGGCCTGCGGGGAGGCCCATACACCCCGAGCCGTCCACTCCAACACGCCCCA

P_AA264959	1755	GGCGAGGAGGCCTGCGGGGAGGCCCATACACCCCGAGCCGTCCACTCCAACACGCCCCA
DNA44804	1607	GTCACCCAGGCCCGCGAGGGCAACCTGCCGCTCCTCATTGCGCCCGCCCTGGCCGCGGTG

P_AA264959	1815	GTCACCCAGGCCCGCGAGGGCAACCTGCCGCTCCTCATTGCGCCCGCCCTGGCCGCGGTG
DNA44804	1667	CTCCTGGCCGCGCTGGCTGCGGTGGGGGCAGCCTACTGTGTGCGGCGGGGCGGGCCATG

P_AA264959	1875	CTCCTGGCCGCGCTGGCTGCGGTGGGGGCAGCCTACTGTGTGCGGCGGGGCGGGCCATG
DNA44804	1727	GCAGCAGCGGCTCAGGACAAAGGGCAGGTGGGGCCAGGGGCTGGGCCCTGGAAGTGGAG

P_AA264959	1935	GCAGCAGCGGCTCAGGACAAAGGGCAGGTGGGGCCAGGGGCTGGGCCCTGGAAGTGGAG
DNA44804	1787	GGAGTGAAGGTCCCCTTGGAGCCAGGCCCAAGGCAACAGAGGGCGGTGGAGAGGCCCTG

P_AA264959	1995	GGAGTGAAGGTCCCCTTGGAGCCAGGCCCAAGGCAACAGAGGGCGGTGGAGAGGCCCTG
DNA44804	1847	CCCAGCGGGTCTGAGTGTGAGGTGCCACTCATGGGCTTCCCAGGGCCTGGCCTCCAGTCA

P_AA264959	2055	CCCAGCGGGTCTGAGTGTGAGGTGCCACTCATGGGCTTCCCAGGGCCTGGCCTCCAGTCA
DNA44804	1907	CCCCTCCACGCAAAGCCCTACATCTAAGCCAGAGAGAGACAGGGCAGCTGGGGCCGGGCT

P_AA264959	2115	CCCCTCCACGCAAAGCCCTACATCTAAGCCAGAGAGAGACAGGGCAGCTGGGGCCGGGCT
DNA44804	1967	CTCAGCCAGTGAGATGGCCAGCCCCCTCCTGCTGCCACACCACGTAAGTTCTCAGTCCCA

P_AA264959	2175	CTCAGCCAGTGAGATGGCCAGCCCCCTCCTGCTGCCACACCACGTAAGTTCTCAGTCCCA
DNA44804	2027	ACCTCGGGGATGTGTGCAGACAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGA

P_AA264959	2235	ACCTCGGGGATGTGTGCAGACAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGA
DNA44804	2087	CCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGA

P_AA264959	2295	CCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAACGTCCCCAGA
DNA44804	2147	ACCGAGTGCCTATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCAC

P_AA264959	2355	ACCGAGTGCCTATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCAC
DNA44804	2207	GGCGGGCCCTGCCATGTGCTGGTAACGCATGCCTGGGCCCTGCTGGGCTCTCCCACTCCA

BLAST RESULTS A-31

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*****
P_AAZ64959 2415 GCGGGGCCCTGCCATGTGCTGGTAACGCATGCCTGGGTCCTGCTGGGCTCTCCCACTCCA
DNA44804 2267 GCGGGACCCTGGGGGCCAGTGAAGGAAGCTCCCGAAAGAGCAGAGGGAGAGCGGGTAGG
*****
P_AAZ64959 2475 GCGGGACCCTGGGGGCCAGTGAAGGAAGCTCCCGAAAGAGCAGAGGGAGAGCGGGTAGG
DNA44804 2327 CGGCTGTGTGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAAGAACTGGAAAGGA
*****
P_AAZ64959 2535 CGGCTGTGTGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAAGAACTGGAAAGGA
DNA44804 2387 AGATGCTTTAGGAACATGTTTTGCTTTTTTAAATATATATATTTATAAGAGATCCTT
*****
P_AAZ64959 2595 AGATGCTTTAGGAACATGTTTTGCTTTTTTAA--ATATATATATTTATAAGAGATCCTT
DNA44804 2447 TCCCATTTATTCTGGGAAGATGTTTTCAAACCTCAGAGACAAGGACTTTGGTTTTTGTA
*****
P_AAZ64959 2653 TCCCATTTATTCTGGGAAGATGTTTTCAAACCTCAGAGACAAGGACTTTGGTTTTTGTA
DNA44804 2507 GACAAACGATGATATGAAGGCCTTTTGTAAGAAAAATAAAA
*****
P_AAZ64959 2713 GACAAACGATGATATGAAGGCCTTTTGTAAGAAAAATAAAA

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Score = 389 (771 bits), Expect = 0.0 [P_AAZ64959, seg 2/2]
Identities = 392/393 (99%), at 18,1-410,393, Strand +/+

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DNA44804 18 ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCGACCCGCCAGGAAAGAC
*****
P_AAZ64959 1 ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCGACCCGCCAGGAAAGAC
DNA44804 78 TGAGGCCGCGGCTGCCCGGCCGCTCCCTGCGCCGCGCGCCTCCCGGGACAGAAGA
*****
P_AAZ64959 61 TGAGGCCGCGGCTGCCCGGCCGCTCCCTGCGCCGCGCGCCTCCCGGGACAGAAGA
DNA44804 138 TGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCTGGGGCCTGGGG
*****
P_AAZ64959 121 TGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCTGGGGCCTGGGG
DNA44804 198 TGCAGGGCTGCCCATCCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTTCTGCACTGCCC
*****
P_AAZ64959 181 TGCAGGGCTGCCCATCCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTTCTGCACTGCCC
DNA44804 258 GCCAGGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGTGGGGCTGTACGTCTTTG
*****
P_AAZ64959 241 GCCAGGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGTGGGGCTGTACGTCTTTG
DNA44804 318 AGAACGGCATCACCATGCTCGACGCAAGCAGCTTTGCCGGCCTGCCGGGCCTGCAGCTCC
*****
P_AAZ64959 301 AGAACGGCATCACCATGCTCGACGCAAGCAGCTTTGCCGGCCTGCCGGGCCTGCAGCTCC
DNA44804 378 TGGACCTGTACAGAACCAGATCGCCAGCCTGC
*****
P_AAZ64959 361 TGGACCTGTACAGAACCAGATCGCCAGCCTGC

```

>11 AX092284 Sequence 15 from Patent WO0116318. (2768 bp) [2 segs]
Score = 2127 (4216 bits), Expect = 0.0 [AX092284, seg 1/2]

BLAST RESULTS A-32

Identities = 2139/2142 (99%), Gaps = 2/2142 (0%), at 407,615-2548,2754, Strand +/+

```
DNA44804      407 CTGCGCCTGCCCCGCCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAG
*****
AX092284      615 CTGCGCCTGCCCCGCCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAG
*****
DNA44804      467 CCGGGCATCCTGGACACTGCCAACGTGGAGGCGCTGCGGCTGGCTGGTCTGGGGCTGCAG
*****
AX092284      675 CCGGGCATCCTGGACACTGCCAACGTGGAGGCGCTGCGGCTGGCTGGTCTGGGGCTGCAG
*****
DNA44804      527 CAGCTGGACGAGGGGCTCTTCAGCCGCTTGCGCAACCTCCACGACCTGGATGTGTCCGAC
*****
AX092284      735 CAGCTGGACGAGGGGCTCTTCAGCCGCTTGCGCAACCTCCACGACCTGGATGTGTCCGAC
*****
DNA44804      587 AACCAGCTGGAGCGAGTGCCACCTGTGATCCGAGGCCTCCGGGGCCTGACGCGCCTGCGG
*****
AX092284      795 AACCAGCTGGAGCGAGTGCCACCTGTGATCCGAGGCCTCCGGGGCCTGACGCGCCTGCGG
*****
DNA44804      647 CTGGCCGGCAACACCCGCATTGCCCAGCTGCGGCCCGAGGACCTGGCCGGCCTGGCTGCC
*****
AX092284      855 CTGGCCGGCAACACCCGCATTGCCCAGCTGCGGCCCGAGGACCTGGCCGGCCTGGCTGCC
*****
DNA44804      707 CTGCAGGAGCTGGATGTGAGCAACCTAAGCCTGCAGGCCCTGCCTGGCGACCTCTCGGGC
*****
AX092284      915 CTGCAGGAGCTGGATGTGAGCAACCTAAGCCTGCAGGCCCTGCCTGGCGACCTCTCGGGC
*****
DNA44804      767 CTCTTCCCCCGCCTGCGGCTGCTGGCAGCTGCCCGCAACCCCTTCAACTGCGTGTGCCCC
*****
AX092284      975 CTCTTCCCCCGCCTGCGGCTGCTGGCAGCTGCCCGCAACCCCTTCAACTGCGTGTGCCCC
*****
DNA44804      827 CTGAGCTGGTTTGGCCCCCTGGGTGCGCGAGAGCCACGTCACACTGGCCAGCCCTGAGGAG
*****
AX092284     1035 CTGAGCTGGTTTGGCCCCCTGGGTGCGCGAGAGCCACGTCACACTGGCCAGCCCTGAGGAG
*****
DNA44804      887 ACGCGCTGCCACTTCCCGCCCAAGAACGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCC
*****
AX092284     1095 ACGCGCTGCCACTTCCCGCCCAAGAACGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCC
*****
DNA44804      947 GACTTTGGCTGCCCAGCCACCACCACAGCCACAGTGCCCAACGAGGCCCGTGGTG
*****
AX092284     1155 GACTTTGGCTGCCCAGCCACCACCACCACAGCCACAGTGCCCAACGAGGCCCGTGGTG
*****
DNA44804     1007 CGGGAGCCCACAGCCTTGCTTCTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCG
*****
AX092284     1215 CGGGAGCCCACAGCCTTGCTTCTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCG
*****
DNA44804     1067 GCCACTGAGGCCCCCAGCCCGCCCTCCACTGCCCCACCGACTGTAGGGCCTGTCCCCAG
*****
AX092284     1275 GCCACTGAGGCCCCCAGCCCGCCCTCCACTGCCCCACCGACTGTAGGGCCTGTCCCCAG
*****
DNA44804     1127 CCCCAGGACTGCCACCGTCCACCTGCCTCAATGGGGGCACATGCCACCTGGGGACACGG
*****
AX092284     1335 CCCCAGGACTGCCACCGTCCACCTGCCTCAATGGGGGCACATGCCACCTGGGGACACGG
*****
DNA44804     1187 CACCACCTGGCGTGCTTGTGCCCCGAAGGCTTCACGGGCCTGTACTGTGAGAGCCAGATG
*****
```

BLAST RESULTS A-33

AX092284	1395	CACCACCTGGCGTGCTTGTGCCCCGAAGGCTTCACGGGCCTGTACTGTGAGAGCCAGATG
DNA44804	1247	GGGCAGGGGACACGGCCCAGCCCTACACCAGTCACGCCGAGGCCACCACGGTCCCTGACC
AX092284	1455	GGGCAGGGGACACGGCCCAGCCCTACACCAGTCACGCCGAGGCCACCACGGTCCCTGACC
DNA44804	1307	CTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGCGTGGGGCTGCAGCGCTACCTCCAG
AX092284	1515	CTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGCGTGGGGCTGCAGCGCTACCTCCAG
DNA44804	1367	GGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCGGGCCCTGAT
AX092284	1575	GGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCGGGCCCTGAT
DNA44804	1427	AAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTGAGTACAGGTCACCCAGCTG
AX092284	1635	AAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTGAGTACAGGTCACCCAGCTG
DNA44804	1487	CGGCCCAACGCCACTTACTCCGTCTGTGTCATGCCTTTGGGGCCCGGGCGGGTGCCGGAG
AX092284	1695	CGGCCCAACGCCACTTACTCCGTCTGTGTCATGCCTTTGGGGCCCGGGCGGGTGCCGGAG
DNA44804	1547	GGCGAGGAGGCCTGCGGGGAGGCCCATACACCCCGAGCCGTCCACTCCAACACGCCCA
AX092284	1755	GGCGAGGAGGCCTGCGGGGAGGCCCATACACCCCGAGCCGTCCACTCCAACACGCCCA
DNA44804	1607	GTCACCCAGGCCCGCGAGGGCAACCTGCCGCTCCTCATTGCGCCCGCCCTGGCCGCGGTG
AX092284	1815	GTCACCCAGGCCCGCGAGGGCAACCTGCCGCTCCTCATTGCGCCCGCCCTGGCCGCGGTG
DNA44804	1667	CTCCTGGCCGCGCTGGCTGCGGTGGGGGAGCCTACTGTGTGCGGCGGGGGCGGGCCATG
AX092284	1875	CTCCTGGCCGCGCTGGCTGCGGTGGGGGAGCCTACTGTGTGCGGCGGGGGCGGGCCATG
DNA44804	1727	GCAGCAGCGGCTCAGGACAAAGGGCAGGTGGGGCCAGGGGCTGGGCCCCTGGAAGTGGAG
AX092284	1935	GCAGCAGCGGCTCAGGACAAAGGGCAGGTGGGGCCAGGGGCTGGGCCCCTGGAAGTGGAG
DNA44804	1787	GGAGTGAAGGTCCCCTTGAGGCCAGGCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTG
AX092284	1995	GGAGTGAAGGTCCCCTTGAGGCCAGGCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTG
DNA44804	1847	CCCAGCGGGTCTGAGTGTGAGGTGCCACTCATGGGCTTCCCAGGGCCTGGCCTCCAGTCA
AX092284	2055	CCCAGCGGGTCTGAGTGTGAGGTGCCACTCATGGGCTTCCCAGGGCCTGGCCTCCAGTCA
DNA44804	1907	CCCCTCCACGCAAAGCCCTACATCTAAGCCAGAGAGAGACAGGGCAGCTGGGGCCGGGCT
AX092284	2115	CCCCTCCACGCAAAGCCCTACATCTAAGCCAGAGAGAGACAGGGCAGCTGGGGCCGGGCT
DNA44804	1967	CTCAGCCAGTGAGATGGCCAGCCCCCTCCTGCTGCCACACCACGTAAGTTCTCAGTCCCA
AX092284	2175	CTCAGCCAGTGAGATGGCCAGCCCCCTCCTGCTGCCACACCACGTAAGTTCTCAGTCCCA
DNA44804	2027	ACCTCGGGGATGTGTGCAGACAGGGCTGTGTGACCACAGCTGGGCCCCTGTTCCCTCTGGA
AX092284	2235	ACCTCGGGGATGTGTGCAGACAGGGCTGTGTGACCACAGCTGGGCCCCTGTTCCCTCTGGA

BLAST RESULTS A-34

DNA44804 2087 CCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCCAGCTGACGAGCCCTAACGTCCCCAGA

 AX092284 2295 CCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCCAGCTGACGAGCCCTAACGTCCCCAGA
 DNA44804 2147 ACCGAGTGCCTATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCAC

 AX092284 2355 ACCGAGTGCCTATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCAC
 DNA44804 2207 GCGGGGCCCTGCCATGTGCTGGTAACGCATGCCTGGGCCCTGCTGGGCTCTCCCACTCCA

 AX092284 2415 GCGGGGCCCTGCCATGTGCTGGTAACGCATGCCTGGGTCCTGCTGGGCTCTCCCACTCCA
 DNA44804 2267 GCGGACCCTGGGGGCCAGTGAAGGAAGCTCCCGGAAAGAGCAGAGGGAGAGCGGGTAGG

 AX092284 2475 GCGGACCCTGGGGGCCAGTGAAGGAAGCTCCCGGAAAGAGCAGAGGGAGAGCGGGTAGG
 DNA44804 2327 CGGCTGTGTGACTCTAGTCTTGCCCCAGGAAGCGAAGGAACAAAAGAACTGGAAAGGA

 AX092284 2535 CGGCTGTGTGACTCTAGTCTTGCCCCAGGAAGCGAAGGAACAAAAGAACTGGAAAGGA
 DNA44804 2387 AGATGCTTTAGGAACATGTTTTGCTTTTTTAAATATATATATATTTATAAGAGATCCTT

 AX092284 2595 AGATGCTTTAGGAACATGTTTTGCTTTTTTAAA--ATATATATATTTATAAGAGATCCTT
 DNA44804 2447 TCCCATTATTCTGGGAAGATGTTTTTCAAACCTCAGAGACAAGGACTTTGGTTTTTGTAA

 AX092284 2653 TCCCATTATTCTGGGAAGATGTTTTTCAAACCTCAGAGACAAGGACTTTGGTTTTTGTAA
 DNA44804 2507 GACAAACGATGATATGAAGGCCTTTTGTAAAGAAAAATAAAA

 AX092284 2713 GACAAACGATGATATGAAGGCCTTTTGTAAAGAAAAATAAAA

Score = 389 (771 bits), Expect = 0.0 [AX092284, seg 2/2]
 Identities = 392/393 (99%), at 18,1-410,393, Strand +/+

DNA44804 18 ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCGACCCGCCAGGAAAGAC

 AX092284 1 ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCGACCCGCCAGGAAAGAC
 DNA44804 78 TGAGGCCGCGGCCTGCCCCGCGCGCTCCCTGCGCCGCGCGCCTCCCGGGACAGAAGA

 AX092284 61 TGAGGCCGCGGCCTGCCCCGCGCGCTCCCTGCGCCGCGCGCCTCCCGGGACAGAAGA
 DNA44804 138 TGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCTGGGGCCTGGGG

 AX092284 121 TGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCTGGGGCCTGGGG
 DNA44804 198 TGCAGGGCTGCCCATCCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTTCTGCACTGCCC

 AX092284 181 TGCAGGGCTGCCCATCCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTTCTGCACTGCCC
 DNA44804 258 GCCAGGGGACCACGGTGGCCCGAGACGTGCCACCCGACACGGTGGGGCTGTACGTCTTTG

 AX092284 241 GCCAGGGGACCACGGTGGCCCGAGACGTGCCACCCGACACGGTGGGGCTGTACGTCTTTG
 DNA44804 318 AGAACGGCATCACCATGCTCGACGCAAGCAGCTTTGCCGGCCTGCCGGGCCTGCAGCTCC

BLAST RESULTS A-35

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*****
AX092284      301 AGAACGGCATCACCATGCTCGACGCAGGCAGCTTTGCCGGCCTGCCGGGCCTGCAGCTCC
DNA44804      378 TGGACCTGTACAGAACCCAGATCGCCAGCCTGC
*****
AX092284      361 TGGACCTGTACAGAACCCAGATCGCCAGCCTGC

>12 P_AAC69514 Human secreted protein gene 3 clone HSYAV50.  DNA, PAT 31-JAN-
2001 (2801 bp) [2 segs]
  Score = 2065 (4094 bits), Expect = 0.0 [P_AAC69514, seg 1/2]
  Identities = 2135/2149 (99%), Gaps = 7/2149 (0%), at 407,650-2555,2791, Strand
  +/+

DNA44804      407 CTGCGCCTGCCCCGCCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAG
*****
P_AAC69514    650 CTGCGCCTGCCCCGCCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAG

DNA44804      467 CCCGGCATCCTGGACACTGCCAACGTGGAGGCGCTGCGGCTGGCTGGTCTGGGGCTGCAG
*****
P_AAC69514    710 CCCGGCATCCTGGACACTGCCAACGTGGAGGCGCTGCGGCTGGCTGGTCTGGGGCTGCAG

DNA44804      527 CAGCTGGACGAGGGGCTCTTCAGCCGCTTGCGCAACCTCCACGACCTGGATGTGTCCGAC
*****
P_AAC69514    770 CAGCTGGACGAGGGGCTCTTCAGCCGCTTGCGCAACCTCCACGACCTGGATGTGTCCGAC

DNA44804      587 AACCAGCTGGAGCGAGTGCCACCTGTGATCCGAGGCCTCCGGGGCCTGACGCGCCTGCGG
*****
P_AAC69514    830 AACCAGCTGGAGCGAGTGCCACCTGTGATCCGAGGCCTCCGGGGCCTGACGCGCCTGCGG

DNA44804      647 CTGGCCGGCAACACCCGCATTGCCAGCTGCGGCCCGAGGACCTGGCCGGCCTGGCTGCC
*****
P_AAC69514    890 CTGGCCGGCAACACCCGCATTGCCAGCTGCGGCCCGAGGACCTGGCCGGCCTGGCTGCC

DNA44804      707 CTGCAGGAGCTGGATGTGAGCAACCTAAGCCTGCAGGCCCTGCCTGGCGACCTCTCGGGC
*****
P_AAC69514    950 CTGCAGGAGCTGGATGTGAGCAACCTAAGCCTGCAGGCCCTGCCTGGCGACCTCTCGGGC

DNA44804      767 CTCTTCCCCCGCCTGCGGCTGCTGGCAGCTGCCCCGAACCCCTTCAACTGCGTGTGCCCC
*****
P_AAC69514   1010 CTCTTCCCCCGCCTGCGGCTGCTGGCAGCTGCCCCGAACCCCTTCAACTGCGTGTGCCCC

DNA44804      827 CTGAGCTGGTTTGGCCCCCTGGGTGCGCGAGAGCCACGTACACTGGCCAGCCCTGAGGAG
*****
P_AAC69514   1070 CTGAGCTGGTTTGGCCCCCTGGGTGCGCGAGAGCCACGTACACTGGCCAGCCCTGAGGAG

DNA44804      887 ACGCGCTGCCACTTCCCGCCCAAGAACGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCC
*****
P_AAC69514   1130 ACGCGCTGCCACTTCCCGCCCAAGAACGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCC

DNA44804      947 GACTTTGGCTGCCCAGCCACCACCACCACAGCCACAGTGCCACACGAGGCCCGTGGTG
*****
P_AAC69514   1190 GACTTTGGCTGCCCAGCCACCACCACCACAGCCACAGTGCCACACGAGGCCCGTGGTG

DNA44804     1007 CGGGAGCCACAGCCTTGTCTTCTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCG
*****
P_AAC69514   1250 CGGGAGCCACAGCCTTGTCTTCTAGCTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCG

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BLAST RESULTS A-30

DNA44804	1067	GCCACTGAGGCCCCCAGCCCGCCCTCCACTGCCCCACCGACTGTAGGGCCTGTCCCCAG

P_AAC69514	1310	GCCACTGAGGCCCCCAGCCCGCCCTCCACTGCCCCACCGACTGTAGGGCCTGTCCCCAG
DNA44804	1127	CCCCAGGACTGCCCACCGTCCACCTGCCTCAATGGGGGCACATGCCACCTGGGGACACGG

P_AAC69514	1370	CCCCAGGACTGCCCACCGTCCACCTGCCTCAATGGGGGCACATGCCACCTGGGGACACGG
DNA44804	1187	CACCACCTGGCGTGCTTGTGCCCCGAAGGCTTCACGGGCCTGTACTGTGAGAGCCAGATG

P_AAC69514	1430	CACCACCTGGCGTGCTTGTGCCCCGAAGGCTTCACGGGCCTGTACTGTGAGAGCCAGATG
DNA44804	1247	GGGCAGGGGACACGGCCCAGCCCTACACCAGTCACGCCGAGGCCACCACGGTCCCTGACC

P_AAC69514	1490	GGGCAGGGGACACGGCCCAGCCCTACACCAGTCACGCCGAGGCCACCACGGTCCCTGACC
DNA44804	1307	CTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGCGTGGGGCTGCAGCGCTACCTCCAG

P_AAC69514	1550	CTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGCGTGGGGCTGCAGCGCTACCTCCAG
DNA44804	1367	GGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCGGGCCCTGAT

P_AAC69514	1610	GGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCGGGCCCTGAT
DNA44804	1427	AAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTCACCCAGCTG

P_AAC69514	1670	AAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTCACCCAGCTG
DNA44804	1487	CGGCCCAACGCCACTTACTCCGTCTGTGTCATGCCTTTGGGGCCCGGGCGGGTGCCGGAG

P_AAC69514	1730	CGGCCCAACGCCACTTACTCCGTCTGTGTCATGCCTTTGGGGCCCGGGCGGGTGCCGGAG
DNA44804	1547	GGCGAGGAGGCCTGCGGGGAGGCCCATACACCCCAAGCCGTCCACTCCAACCACGCCCCA

P_AAC69514	1790	GGCGAGGAGGCCTGCGGGGAGGCCCATACACCCCAAGCCGTCCACTCCAACCACGCCCCA
DNA44804	1607	GTCACCCAGGCCCGCGAGGGCAACCTGCCGCTCCTCATTGCGCCCGCCCTGGCCGCGGTG

P_AAC69514	1850	GTCACCCAGGCCCGCGAGGGCAACCTGCCGCTCCTCATTGCGCCCGCCCTGGCCGCGGTG
DNA44804	1667	CTCCTGGCCGCGCTGGCTGCGGTGGGGGCAGCCTACTGTGTGCGGCGGGGGCGGGCCATG

P_AAC69514	1910	CTCCTGGCCGCGCTGGCTGCGGTGGGGGCAGCCTACTGTGTGCGGCGGGGGCGGGCCATG
DNA44804	1727	GCAGCAGCGGCTCAGGACAAAGGGCAGGTGGGGCCAGGGGCTGGGCCCTGGAAGTGGAG

P_AAC69514	1970	GCAGCAGCGGCTCAGGACAAAGGGCAGGTGGGGCCAGGGGCTGGGCCCTGGAAGTGGAG
DNA44804	1787	GGAGTGAAGGTCCCCTTGAGGCCAGGCCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTG

P_AAC69514	2030	GGAGTGAAGGTCCCCTTGAGGCCAGGCCCGAAGGCAACAGA-GGCGGTGGAGAGGCCCTG
DNA44804	1847	CCCAGCGGGTCTGAGTGTGAGGTGCCACTCATGGGCTTCCCAGGGCCTGGCCTCCAGTCA

P_AAC69514	2089	CCCAGCGGGTCTGAGTGTGAGGTGCCACTCATGGGCTT-CCAAGGCCTGGCCT-CAGTCA
DNA44804	1907	CCCCTCCACGCAAAGCCCTACATCTAAGCCAGAGAGAGACAGGGCAGCTGGGGCCGGGCT

BLAST RESULTS A-37

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*****
P_AAC69514 2147 CCCCTTCACGCAAAGCCCTACATCTAAGCCAGAGAGACAGGGCAGCT-GGGCCGGG-T
DNA44804 1967 CTCAGCCAGTGAGATGGCCAGCCCCCTCCTGCTGCCACACCACGTAAGTTCTCAGTCCCA
*****
P_AAC69514 2205 TTCAGCCAGTGAGAT-GCCAGCCCCCTTCCTGCTGCCACACCACGTAAGTTCTCAGTCCCA
DNA44804 2027 ACCTCGGGGATGTGTGCAGACAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCTCTGGA
*****
P_AAC69514 2264 ACCTCGGGGATGTGTGCAGACAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCTCTGGA
DNA44804 2087 CCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCCAGCTGACGAGCCCTAACGTCCCCAGA
*****
P_AAC69514 2324 CCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCCAGCTGACGAGCCCTAACGTCCCCAGA
DNA44804 2147 ACCGAGTGCCTATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCAC
*****
P_AAC69514 2384 ACCGAGTGCCTATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCAC
DNA44804 2207 GGCGGGCCCTGCCATGTGCTGGTAACGCATGCCTGGGCCCTGCTGGGCTCTCCCACTCCA
*****
P_AAC69514 2444 GGCGGG-CCTGCCATGTGCTGGTAACGCATGCCTGGGCCCTGCTGGGCTCTCCCACTCCA
DNA44804 2267 GGCGGACCCTGGGGGCCAGTGAAGGAAGCTCCCGAAAGAGCAGAGGGAGAGCGGGTAGG
*****
P_AAC69514 2503 GGCGGACCCTGGGGGCCAGTGAAGGAAGCTCCCGAAAGAGCAGAGGGAGAGCGGGTAGG
DNA44804 2327 CGGCTGTGTGACTCTAGTCTTGCCCCAGGAAGCGAAGGAACAAAAGAACTGGAAAGGA
*****
P_AAC69514 2563 CGGCTGTGTGACTCTAGTCTTGCCCCAGGAAGCGAAGGAACAAAAGAACTGGAAAGGA
DNA44804 2387 AGATGCTTTAGGAACATGTTTTGCTTTTTTAAATATATATATATTTATAAGAGATCCTT
*****
P_AAC69514 2623 AGATGCTTTAGGAACATGTTTTGCTTTTTTAAATATATATATATTTATAAGAGATCCTT
DNA44804 2447 TCCCATTTATTCTGGGAAGATGTTTTTCAAACCTCAGAGACAAGGACTTTGGTTTTTGTA
*****
P_AAC69514 2683 TCCCATTTATTCTGGGAAGATGTTTTTCAAACCTCAGAGACAAGGACTTTGGTTTTTGTA
DNA44804 2507 GACAAACGATGATATGAAGGCCTTTTGTAAAGAAAAATAAAAAAAAAA
*****
P_AAC69514 2743 GACAAACGATGATATGAAGGCCTTTTGTAAAGAAAAATAAAAAAAAAA

```

Score = 406 (805 bits), Expect = 0.0 [P_AAC69514, seg 2/2]
Identities = 409/410 (99%), at 1,19-410,428, Strand +/-

```

DNA44804 1 GGGGCGGGTGGACGCGGACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCC
*****
P_AAC69514 19 GGGGCGGGTGGACGCGGACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCC
DNA44804 61 GACCCGCCAGGAAAGACTGAGGCCGCGGCCTGCCCCGCGCGGCTCCCTGCGCCGCCGCCG
*****
P_AAC69514 79 GACCCGCCAGGAAAGACTGAGGCCGCGGCCTGCCCCGCGCGGCTCCCTGCGCCGCCGCCG
DNA44804 121 CCTCCCGGGACAGAAGATGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACT
*****
P_AAC69514 139 CCTCCCGGGACAGAAGATGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACT

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BLAST RESULTS A-38

DNA44804	181	GGCCCTGGGGCCTGGGGTGCAGGGCTGCCCATCCGGCTGCCAGTGCAGCCAGCCACAGAC

P_AAC69514	199	GGCCCTGGGGCCTGGGGTGCAGGGCTGCCCATCCGGCTGCCAGTGCAGCCAGCCACAGAC
DNA44804	241	AGTCTTCTGCACTGCCCCGCCAGGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGT

P_AAC69514	259	AGTCTTCTGCACTGCCCCGCCAGGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGT
DNA44804	301	GGGGCTGTACGTCTTTGAGAACGGCATCACCATGCTCGACGCAAGCAGCTTTGCCGGCCT

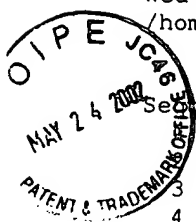
P_AAC69514	319	GGGGCTGTACGTCTTTGAGAACGGCATCACCATGCTCGACGCAAGCAGCTTTGCCGGCCT
DNA44804	361	GCCGGGCCTGCAGCTCCTGGACCTGTCACAGAACCAGATCGCCAGCCTGC

P_AAC69514	379	GCCGGGCCTGCAGCTCCTGGACCTGTCACAGAACCAGATCGCCAGCCTGC

BLAST RESULTS A-39

(2)

Wed Aug 29 08:13:54 2001 [BLASTP 2.1.3 [Apr-1-2001], NCBI]
/home/ruby/va/Molbio/carpanda/tempids/pl.DNA44804 (598 aa)



Sequences producing High-scoring Segment Pairs:

		Score	Match	Pct	E-val
1	P_AAB01322 Human PRO357 polypeptide - Homo sapiens.	3135	598	100	0.0
2	P_AAY93691 novel polypeptide PRO357 - Homo sapiens.	3135	598	100	0.0
3	P_AAY06484 Human tumour-associated protein PRO357 -	3135	598	100	0.0
4	P_AAY17831 Human PRO357 protein sequence - Homo sapi	3126	597	100	0.0
5	P_AAB65166 Human PRO1282 (UNQ652) protein sequence S	2946	582	86	0.0
6	P_AAB87533 Human PRO1282 - Homo sapiens.	2946	582	86	0.0
7	P_AAB07428 leucine-rich surface glycoprotein (LRSG)	2946	582	86	0.0
8	CAC49977.1 unnamed protein product - Homo sapiens	2941	581	86	0.0
9	P_AAB38400 Fragment of human secreted protein encode	2792	560	83	0.0
10	P_AAB38323 Human secreted protein encoded by gene 3	2792	560	83	0.0
11	P_AAY66643 Membrane-bound protein PRO1282 - Homo sap	2405	502	75	0.0

>1 P_AAB01322 Human PRO357 polypeptide - Homo sapiens. (598 aa) [1 seg]
Score = 3135 (1212 bits), Expect = 0.0
Identities = 598/598 (100%), Positives = 598/598 (100%), at 1,1-598,598

DNA44804	1	MCSRVP L L L L L L L L L L L A L G P G V Q G C P S G C Q C S Q P Q T V F C T A R Q G T T V P R D V P P D T V G L Y V F
P_AAB01322	1	MCSRVP L L L L L L L L L L L A L G P G V Q G C P S G C Q C S Q P Q T V F C T A R Q G T T V P R D V P P D T V G L Y V F
DNA44804	61	ENGITMLDASSFAGLPGLQLLDLSQNQIASRLRPRLLLLDLSHNSLLALEPGILDANVE
P_AAB01322	61	ENGITMLDASSFAGLPGLQLLDLSQNQIASRLRPRLLLLDLSHNSLLALEPGILDANVE
DNA44804	121	ALRLAGLGLQQLDEGLFSRLRNLDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQL
P_AAB01322	121	ALRLAGLGLQQLDEGLFSRLRNLDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQL
DNA44804	181	RPEDLAGLAALQELDVSNSLSLQALPGDLSGLFPRLRLLAAARNPFNCVCPLSWFGPWVRE
P_AAB01322	181	RPEDLAGLAALQELDVSNSLSLQALPGDLSGLFPRLRLLAAARNPFNCVCPLSWFGPWVRE
DNA44804	241	SHVTLASPEETRCHFPKPNAGRLLELDYADFGCPATTTTATVPTRPVVREPTALSSSL
P_AAB01322	241	SHVTLASPEETRCHFPKPNAGRLLELDYADFGCPATTTTATVPTRPVVREPTALSSSL
DNA44804	301	APTWLSPTAPATEAPSPSTAPPTVGVPVQPQDCPPSTCLNGGTCHLGRHHLACLCEP
P_AAB01322	301	APTWLSPTAPATEAPSPSTAPPTVGVPVQPQDCPPSTCLNGGTCHLGRHHLACLCEP
DNA44804	361	FTGLYCESQMGQTRPSPTPVTPRPPRSLT LGIEPVSP TSLRVGLQRYLQGSSVQLRSLR
P_AAB01322	361	FTGLYCESQMGQTRPSPTPVTPRPPRSLT LGIEPVSP TSLRVGLQRYLQGSSVQLRSLR
DNA44804	421	LTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCMPLGPGRVPEGEEACGEAHT
P_AAB01322	421	LTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCMPLGPGRVPEGEEACGEAHT
DNA44804	481	PPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALA AVGAAYCVR RGRAMAAAAQDKGV
P_AAB01322	481	PPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALA AVGAAYCVR RGRAMAAAAQDKGV

BLAST RESULTS B-1

DNA44804 541 GPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGPGLQSPLHAKPYI

 P_AAB01322 541 GPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGPGLQSPLHAKPYI

>2 P_AAY93691 novel polypeptide PRO357 - Homo sapiens. (598 aa) [1 seg]
 Score = 3135 (1212 bits), Expect = 0.0
 Identities = 598/598 (100%), Positives = 598/598 (100%), at 1,1-598,598

DNA44804 1 MCSRVPLLLPLLLLLLALGPGVQCPSGCQCSQPQTVFCTARQGTTPRDVPPDVTGLYVF

 P_AAY93691 1 MCSRVPLLLPLLLLLLALGPGVQCPSGCQCSQPQTVFCTARQGTTPRDVPPDVTGLYVF

DNA44804 61 ENGITMLDASSFAGLPGLQLLDLSQNQIASLRLPRLLLLDLSHNSLLALEPGILDANVE

 P_AAY93691 61 ENGITMLDASSFAGLPGLQLLDLSQNQIASLRLPRLLLLDLSHNSLLALEPGILDANVE

DNA44804 121 ALRLAGLGLQQLDEGLFSRLRNLDLSDVSDNQLERVPPVIRGLRGLTRRLAGNTRIAQL

 P_AAY93691 121 ALRLAGLGLQQLDEGLFSRLRNLDLSDVSDNQLERVPPVIRGLRGLTRRLAGNTRIAQL

DNA44804 181 RPEDLAGLAALQELDVSNSLSQALPGDLSGLFPRLRLAAARNPFNCVCPLSWFGPWVRE

 P_AAY93691 181 RPEDLAGLAALQELDVSNSLSQALPGDLSGLFPRLRLAAARNPFNCVCPLSWFGPWVRE

DNA44804 241 SHVTLASPEETRCHFPKKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL

 P_AAY93691 241 SHVTLASPEETRCHFPKKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL

DNA44804 301 APTWLSPTAPATEAPSPSTAPPTVGPVPQPDCCPSTCLNGGTCHLGRHHLACLCEP

 P_AAY93691 301 APTWLSPTAPATEAPSPSTAPPTVGPVPQPDCCPSTCLNGGTCHLGRHHLACLCEP

DNA44804 361 FTGLYCESQMGQGRPSPTPVTPRPPRSLTLGIEFVSPTSLSRVGLQRYLQSSVQLRSLR

 P_AAY93691 361 FTGLYCESQMGQGRPSPTPVTPRPPRSLTLGIEFVSPTSLSRVGLQRYLQSSVQLRSLR

DNA44804 421 LTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCMPLGPGRVPEGEEACGEAHT

 P_AAY93691 421 LTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCMPLGPGRVPEGEEACGEAHT

DNA44804 481 PPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAGAAVCVRRGRAMAAAAQDKGQV

 P_AAY93691 481 PPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAGAAVCVRRGRAMAAAAQDKGQV

DNA44804 541 GPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGPGLQSPLHAKPYI

 P_AAY93691 541 GPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGPGLQSPLHAKPYI

>3 P_AAY06484 Human tumour-associated protein PRO357 - Homo sapiens. (598 aa) [1 seg]
 Score = 3135 (1212 bits), Expect = 0.0
 Identities = 598/598 (100%), Positives = 598/598 (100%), at 1,1-598,598

DNA44804 1 MCSRVPLLLPLLLLLLALGPGVQCPSGCQCSQPQTVFCTARQGTTPRDVPPDVTGLYVF

 P_AAY06484 1 MCSRVPLLLPLLLLLLALGPGVQCPSGCQCSQPQTVFCTARQGTTPRDVPPDVTGLYVF

BLAST RESULTS 8-2

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DNA44804 61 ENGITMLDASSFAGLPGLQLLDLSQNQIASLRLPRLLLLDLSHNSLLALEPGILDTANVE
*****
P_AAY06484 61 ENGITMLDASSFAGLPGLQLLDLSQNQIASLRLPRLLLLDLSHNSLLALEPGILDTANVE

DNA44804 121 ALRLAGLGLQQLDEGLFSRLRNLDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQL
*****
P_AAY06484 121 ALRLAGLGLQQLDEGLFSRLRNLDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQL

DNA44804 181 RPEDLAGLAALQELDVSNSLSLQALPGDLSGLFPRLRLAAARNPFNCVCPLSWFGPWVRE
*****
P_AAY06484 181 RPEDLAGLAALQELDVSNSLSLQALPGDLSGLFPRLRLAAARNPFNCVCPLSWFGPWVRE

DNA44804 241 SHVTLASPEETRCHFPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL
*****
P_AAY06484 241 SHVTLASPEETRCHFPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL

DNA44804 301 APTWLSPTAPATEAPSPSTAPPTVGVPVQPQDCPPSTCLNGGTCHLGRHHLACLCEP
*****
P_AAY06484 301 APTWLSPTAPATEAPSPSTAPPTVGVPVQPQDCPPSTCLNGGTCHLGRHHLACLCEP

DNA44804 361 FTGLYCESQMGGTRPSPTVTPRPPRSLTGIEPVSPTSLRVGLQRYLQGSSVQLRSLR
*****
P_AAY06484 361 FTGLYCESQMGGTRPSPTVTPRPPRSLTGIEPVSPTSLRVGLQRYLQGSSVQLRSLR

DNA44804 421 LTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCMPLGPGRVPEGEEACGEAHT
*****
P_AAY06484 421 LTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCMPLGPGRVPEGEEACGEAHT

DNA44804 481 PPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRGRAMAAAAQDKGQV
*****
P_AAY06484 481 PPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAVGAAYCVRGRAMAAAAQDKGQV

DNA44804 541 GPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGPGLQSPLHAKPYI
*****
P_AAY06484 541 GPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGPGLQSPLHAKPYI

>4 P_AAY17831 Human PRO357 protein sequence - Homo sapiens. (598 aa) [1 seg]
Score = 3126 (1208 bits), Expect = 0.0
Identities = 597/598 (99%), Positives = 597/598 (99%), at 1,1-598,598

DNA44804 1 MCSRVPLLLPLLLLLALGPGVQCPSGCQCSQPQTVFCTARQGTTVPRDVPPDVTGLYVE
*****
P_AAY17831 1 MCSRVPLLLPLLLLLALGPGVQCPSGCQCSQPQTVFCTARQGTTVPRDVPPDVTGLYVE

DNA44804 61 ENGITMLDASSFAGLPGLQLLDLSQNQIASLRLPRLLLLDLSHNSLLALEPGILDTANVE
*****
P_AAY17831 61 ENGITMLDASSFAGLPGLQLLDLSQNQIASLRLPRLLLLDLSHNSLLALEPGILDTANVE

DNA44804 121 ALRLAGLGLQQLDEGLFSRLRNLDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQL
*****
P_AAY17831 121 ALRLAGLGLQQLDEGLFSRLRNLDLDVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQL

DNA44804 181 RPEDLAGLAALQELDVSNSLSLQALPGDLSGLFPRLRLAAARNPFNCVCPLSWFGPWVRE
*****
P_AAY17831 181 RPEDLAGLAALQELDVSNSLSLQALPGDLSGLFPRLRLAAARNPFNCVCPLSWFGPWVRE

DNA44804 241 SHVTLASPEETRCHFPKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSL

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BLAST RESULTS B-3

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*****
P_AAY17831 241 SHVTLASPEETRCHFPKKNAGRLLELDYADFGCPATTTTATVPTRPVVREPTALSSSL
DNA44804 301 APTWLSPTAPATEAPSPSTAPPTVGPVQPQDCPPSTCLNGGTCHLGRHHLACLCPEG
*****
P_AAY17831 301 APTWLSPTAPATEAPSPSTAPPTVGPVQPQDCPPSTCLNGGTCHLGRHHLACLCPEG
DNA44804 361 FTGLYCESQMGQTRPSPTPVTPRPPRSLTLGIEPVSPTSLRVGLQRYLQGSSVQLRSLR
*****
P_AAY17831 361 FTGLYCESQMGQTRPSPTPVTPRPPRSLTLGIEPVSPTSLRVGLQRYLQGSSVQLRSLR
DNA44804 421 LTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCMPLGPGRVPEGEEACGEAHT
*****
P_AAY17831 421 LTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCMPLGPGRVPEGEEACGEAHT
DNA44804 481 PPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAGAAVCVRRGRAMAAAAQDKGQV
*****
P_AAY17831 481 PPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAGAAVCVRRGRAMAAAAQDKGQV
DNA44804 541 GPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGPGLQSPLHAKPYI
*****
P_AAY17831 541 GPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGPGLQSPLHAKPYI

```

>5 P_AAB65166 Human PRO1282 (UNQ652) protein sequence SEQ ID NO:52 - Homo (673 aa) [1 seg]
 Score = 2946 (1139 bits), Expect = 0.0
 Identities = 582/673 (86%), Positives = 588/673 (86%), Gaps = 75/673 (11%), at 1,1-598,673

```

DNA44804 1 MCSRVPLLLPLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTPRDVPPDTVGLYVF
*****
P_AAB65166 1 MCSRVPLLLPLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTPRDVPPDTVGLYVF
DNA44804 61 EN-----GITMLDAS-----SF
** * . * * *
P_AAB65166 61 ENGITMLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETF
DNA44804 73 AGLPGLQLLDLSQNQIAS-----LRLPRLLLLDLSHNS
** * . * * *
P_AAB65166 121 RGLRRLERLYLGKNRIRHIQPGAFDTLDRLELKLQDNELRALPPLRLPRLLLLDLSHNS
DNA44804 106 LLALEPGILDTANVEALRLAGLGLQQLDEGLFSRLRLNLHDLVDSDNQLERVPPVIRGLRG
*****
P_AAB65166 181 LLALEPGILDTANVEALRLAGLGLQQLDEGLFSRLRLNLHDLVDSDNQLERVPPVIRGLRG
DNA44804 166 LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNSLSLQALPGDLSGLFPRLRLAAARNPF
*****
P_AAB65166 241 LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNSLSLQALPGDLSGLFPRLRLAAARNPF
DNA44804 226 NVCPLSWFGPWVRESHVTLASPEETRCHFPKKNAGRLLELDYADFGCPATTTTATVPT
*****
P_AAB65166 301 NVCPLSWFGPWVRESHVTLASPEETRCHFPKKNAGRLLELDYADFGCPATTTTATVPT
DNA44804 286 TRPVVREPTALSSSLAPTWLSPTAPATEAPSPSTAPPTVGPVQPQDCPPSTCLNGGTC
*****
P_AAB65166 361 TRPVVREPTALSSSLAPTWLSPTAPATEAPSPSTAPPTVGPVQPQDCPPSTCLNGGTC

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BLAST RESULTS 8-4

```

DNA44804 346 HLGTRHHLACLCPEGFTGLYCESQMGQGRPSPTPVTPRPPRSLTLGIEPVSPTSRLVGL
*****
P_AAB65166 421 HLGTRHHLACLCPEGFTGLYCESQMGQGRPSPTPVTPRPPRSLTLGIEPVSPTSRLVGL
*****
DNA44804 406 QRYLQGSSVQLRSLRLTYRNLSGDPKRLVTLRLPASLAEYTVTQLRPNATYSVCMPLGP
*****
P_AAB65166 481 QRYLQGSSVQLRSLRLTYRNLSGDPKRLVTLRLPASLAEYTVTQLRPNATYSVCMPLGP
*****
DNA44804 466 GRVPEGEEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAGVGAAYCVR
*****
P_AAB65166 541 GRVPEGEEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAGVGAAYCVR
*****
DNA44804 526 RGRAMAAAAQDKGQVGPAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFP
*****
P_AAB65166 601 RGRAMAAAAQDKGQVGPAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFP
*****
DNA44804 586 PGLQSPLHAKPYI
*****
P_AAB65166 661 PGLQSPLHAKPYI
*****
>6 P_AAB87533 Human PRO1282 - Homo sapiens. (673 aa) [1 seg]
Score = 2946 (1139 bits), Expect = 0.0
Identities = 582/673 (86%), Positives = 588/673 (86%), Gaps = 75/673 (11%), at
1,1-598,673

DNA44804 1 MCSRVPLLLPLLLLLLALGPGVQGPCSGCQCSQPQTVFCTARQGTTPRDPVPPDTVGLYVF
*****
P_AAB87533 1 MCSRVPLLLPLLLLLLALGPGVQGPCSGCQCSQPQTVFCTARQGTTPRDPVPPDTVGLYVF
*****
DNA44804 61 EN-----GITMLDAS-----SF
** * . * * *
P_AAB87533 61 ENGITMLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETF
*****
DNA44804 73 AGLPGLQLLDLSQNQIAS-----LRLPRLLLLDLSHNS
** * . * * *
P_AAB87533 121 RGLRRLERLYLGKNRIRHIQPGAFDTLDRLLELKLQDNELRALPPLRLPRLLLLDLSHNS
*****
DNA44804 106 LLALEPGILDANVEALRLAGLGLQQLDEGLFSRLRNLDLDVSDNQLERVPPVIRGLRG
*****
P_AAB87533 181 LLALEPGILDANVEALRLAGLGLQQLDEGLFSRLRNLDLDVSDNQLERVPPVIRGLRG
*****
DNA44804 166 LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLAAARNPF
*****
P_AAB87533 241 LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNLSLQALPGDLSGLFPRLRLAAARNPF
*****
DNA44804 226 NCVCPLSWFGPWVRESHVTLASPEETRCHFPKNAGRLLLELDYADFGCPATTTTATVPT
*****
P_AAB87533 301 NCVCPLSWFGPWVRESHVTLASPEETRCHFPKNAGRLLLELDYADFGCPATTTTATVPT
*****
DNA44804 286 TRPVVREPTALSSSLAPTWLSPTAPATEAPSPSTAPPTVGPVPQPDCCPSTCLNGGTC
*****
P_AAB87533 361 TRPVVREPTALSSSLAPTWLSPTAPATEAPSPSTAPPTVGPVPQPDCCPSTCLNGGTC
*****
DNA44804 346 HLGTRHHLACLCPEGFTGLYCESQMGQGRPSPTPVTPRPPRSLTLGIEPVSPTSRLVGL
*****
P_AAB87533 421 HLGTRHHLACLCPEGFTGLYCESQMGQGRPSPTPVTPRPPRSLTLGIEPVSPTSRLVGL
*****

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BLAST RESULTS B-5

DNA44804 406 QRYLQGSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCMPLGP

 P_AAB87533 481 QRYLQGSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCMPLGP

 DNA44804 466 GRVPEGEEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAGVGAAYCVR

 P_AAB87533 541 GRVPEGEEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAGVGAAYCVR

 DNA44804 526 RGRAMAAAQDKGQVGPAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFP

 P_AAB87533 601 RGRAMAAAQDKGQVGPAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFP

 DNA44804 586 PGLQSPLHAKPYI

 P_AAB87533 661 PGLQSPLHAKPYI

>7 P_AAB07428 leucine-rich surface glycoprotein (LRSG) - Homo sapiens. (673 aa)
 [1 seg]
 Score = 2946 (1139 bits), Expect = 0.0
 Identities = 582/673 (86%), Positives = 588/673 (86%), Gaps = 75/673 (11%), at
 1,1-598,673

DNA44804 1 MCSRVPLLLPLLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTPRDPVPPDTVGLYVF

 P_AAB07428 1 MCSRVPLLLPLLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTPRDPVPPDTVGLYVF

 DNA44804 61 EN-----GITMLDAS-----SF
 ** * . * * *
 P_AAB07428 61 ENGITMLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETF

 DNA44804 73 AGLPGLQLLDLSQNQIAS-----LRLPRLLLLDLSHNS
 ** * . * * *
 P_AAB07428 121 RGLRRLRLYLGNRIRHIQPGAFDTLDRLLELKLQDNELRALPPLRLPRLLLLDLSHNS

 DNA44804 106 LLALEPGILDTANVEALRLAGLGLQQLDEGLFSRLRNLDLDVSDNQLERVPPVIRGLRG

 P_AAB07428 181 LLALEPGILDTANVEALRLAGLGLQQLDEGLFSRLRNLDLDVSDNQLERVPPVIRGLRG

 DNA44804 166 LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNSLQALPGDLSGLFPRLRLLLAAARNPF

 P_AAB07428 241 LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNSLQALPGDLSGLFPRLRLLLAAARNPF

 DNA44804 226 NCVCPLSWFGPWVRESHVTLASPEETRCHFPKPNAGRLLELDYADFGCPATTTTATVPT

 P_AAB07428 301 NCVCPLSWFGPWVRESHVTLASPEETRCHFPKPNAGRLLELDYADFGCPATTTTATVPT

 DNA44804 286 TRPVVREPTALSSSLAPTWSPTAPATEAPSPPSTAPPTVGVPVQPQDCPPSTCLNGGTC

 P_AAB07428 361 TRPVVREPTALSSSLAPTWSPTAPATEAPSPPSTAPPTVGVPVQPQDCPPSTCLNGGTC

 DNA44804 346 HLGTRHHLACLCPEGFTGLYCESQMGQTRPSPTPVTPRPPRSLTGIEPVSPTSRLVGL

 P_AAB07428 421 HLGTRHHLACLCPEGFTGLYCESQMGQTRPSPTPVTPRPPRSLTGIEPVSPTSRLVGL

 DNA44804 406 QRYLQGSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCMPLGP

 P_AAB07428 481 QRYLQGSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCMPLGP

BLAST RESULTS B-C

DNA44804 466 GRVPEGEEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAGVGAAYCVR

 P_AAB07428 541 GRVPEGEEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAGVGAAYCVR
 DNA44804 526 RGRAMAAAQDKGQVGPAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPG

 P_AAB07428 601 RGRAMAAAQDKGQVGPAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPG
 DNA44804 586 PGLQSPLHAKPYI

 P_AAB07428 661 PGLQSPLHAKPYI

>8 CAC49977.1 unnamed protein product - Homo sapiens (673 aa) [1 seg]
 Score = 2941 (1137 bits), Expect = 0.0
 Identities = 581/673 (86%), Positives = 587/673 (86%), Gaps = 75/673 (11%), at
 1,1-598,673

DNA44804 1 MCSRVPLLLPLLLLLALGPGVQGCPSGCQCSQPQTVECTARQGTTPRDPVPPDTVGLYVF

 CAC49977.1 1 MCSRVPLLLPLLLLLALGPGVQGCPSGCQCSQPQTVECTARQGTTPRDPVPPDTVGLYVF
 DNA44804 61 EN-----GITMLDAS-----SF
 ** * . ** *
 CAC49977.1 61 ENGITMLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETF
 DNA44804 73 AGLPGLQLLDLSQNQIAS-----LRLPRLLLLDLSHNS
 ** * . * * . *
 CAC49977.1 121 RGLRRLERLYLGKNRIRHIQPGAFDTLDRLLELKLQDNELRALPPLRLPRLLLLDLSHNS
 DNA44804 106 LLALEPGILDTANVEALRLAGLGLQQLDEGLFSRLRNLDLDVSDNQLERVPPVIRGLRG

 CAC49977.1 181 LLALEPGILDTANVEALRLAGLGLQQLDEGLFSRLRNLDLDVSDNQLERVPPVIRGLRG
 DNA44804 166 LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNSLSLQALPGDLSGLFPRLRLAAARNPF

 CAC49977.1 241 LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNSLSLQALPGDLSGLFPRLRLAAARNPF
 DNA44804 226 NCVCPLSWFGPWVRESHVTLASPEETRCHFPKNAGRLLLELDYADFGCPATTTTATVPT

 CAC49977.1 301 NCVCPLSWFGPWVRESHVTLASPEETRCHFPKNAGRLLLELDYADFGCPATTTTATVPT
 DNA44804 286 TRPVVREPTALSSSLAPTWLSPTAPATEAPSPSTAPPTVGPVPQPQDCPPSTCLNGGTC

 CAC49977.1 361 TRPVVREPTALSSSLAPTWLSPTAPATEAPSPSTAPPTVGPVPQPQDCPPSTCLNGGTC
 DNA44804 346 HLGTRHHLACLCEGFTGLYCESQMGQTRPSPTPVTPRPPRSLTGLIEPVSPTSRLRVGL

 CAC49977.1 421 HLGTRHHLACLCEGFTGLYCESQMGQTRPSPTPVTPRPPRSLTGLIEPVSPTSRLRVGL
 DNA44804 406 QRYLQGSSVQLRSLRLTYRNLSPGDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGP

 CAC49977.1 481 QRYLQGSSVQLRSLRLTYRNLSPGDKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGP
 DNA44804 466 GRVPEGEEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAGVGAAYCVR

 CAC49977.1 541 GRVPEGEEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAGVGAAYCVR

BLAST RESULTS B-7

DNA44804 526 RGRAMAAAAQDKGQVGPAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPG

 CAC49977.1 601 RGRAMAAAAQDKGQVGPAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPG

 DNA44804 586 PGLQSPLHAKPYI

 CAC49977.1 661 PGLQSPLHAKPYI

>9 P_AAB38400 Fragment of human secreted protein encoded by gene 3 clone HSYAV50
 - Homo sapiens. (723 aa) [1 seg]
 Score = 2792 (1080 bits), Expect = 0.0
 Identities = 560/673 (83%), Positives = 568/673 (84%), Gaps = 76/673 (11%), at
 1,52-598,723

DNA44804 1 MCSRVPLLLPLLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTPRDPVPPDTVGLYVF

 P_AAB38400 52 MCSRVPLLLPLLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTPRDPVPPDTVGLYVF

DNA44804 61 EN-----GITMLDAS-----SF
 ** * . * * *
 P_AAB38400 112 ENGITMLDAGSFAGLPGQLLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETF

DNA44804 73 AGLPGLQLLDLSQNQIAS-----LRLPRLLLLDLSHNS
 ** * . * * . * *
 P_AAB38400 172 RGLRRLERLYLGKNRIRHIQPGAFDTLDRLLELKLQDNELRALPPLRLPRLLLLDLSHNS

DNA44804 106 LLALEPGILDANVEALRLAGLGLQQLDEGLFSRLRLNLHDLVDSDNQLERVPPVIRGLRG

 P_AAB38400 232 LLALEPGILDANVEALRLAGLGLQQLDEGLFSRLRLNLHDLVDSDNQLERVPPVIRGLRG

DNA44804 166 LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNSLSLQALPGDLSGLFPRLRLLLAAARNPF

 P_AAB38400 292 LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNSLSLQALPGDLSGLFPRLRLLLAAARNPF

DNA44804 226 NCVCPLSWFGPWVRESHVTLASPEETRCHFPKRNAGRLLELDYADFGCPATTTTATVPT

 P_AAB38400 352 NCVCPLSWFGPWVRESHVTLASPEETRCHFPKRNAGRLLELDYADFGCPATTTTATVPT

DNA44804 286 TRPVVREPTALSSSLAPTWLSPTAPATEAPSPPSTAPPTVGPVPQPDCCPPSTCLNGGTC

 P_AAB38400 412 TRPVVREPTALSSSLAPTWLSPTAPATEAPSPPSTAPPTVGPVPQPDCCPPSTCLNGGTC

DNA44804 346 HLGTRHHLACLCEGFTGLYCESQMGQTRPSPTPVTPRPPRSLTGIEPVSPTSLSRVGL

 P_AAB38400 472 HLGTRHHLACLCEGFTGLYCESQMGQTRPSPTPVTPRPPRSLTGIEPVSPTSLSRVGL

DNA44804 406 QRYLQGSSVQLRSLRLTYRNLSGDPKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGP

 P_AAB38400 532 QRYLQGSSVQLRSLRLTYRNLSGDPKRLVTLRLPASLAEYTVTQLRPNATYSVCVMPLGP

DNA44804 466 GRVPEGEEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAGVGAAYCVR

 P_AAB38400 592 GRVPEGEEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAGVGAAYCVR

DNA44804 526 RGRAMAAAAQDKGQVGPAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPG

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P_AAB38400 652 RGRAMAAAAQDKGVGPGAGPLELEGVKVPLEPGPKATEAVERPCPAGLSVKCHSWASKA
DNA44804 586 PGLQSPLHAKPYI

P_AAB38400 712 -WPQSPLHAKPYI

>10 P_AAB38323 Human secreted protein encoded by gene 3 clone HSYAV50 - Homo
(673 aa) [1 seg]
Score = 2792 (1080 bits), Expect = 0.0
Identities = 560/673 (83%), Positives = 568/673 (84%), Gaps = 76/673 (11%), at
1,1-598,672

DNA44804 1 MCSRVPLLLPLLLLLALGPGVQGCPSGCQCSQPQTTFCTARQGTTPRDPVPPDVTGLYVF

P_AAB38323 1 MCSRVPLLLPLLLLLALGPGVQGCPSGCQCSQPQTTFCTARQGTTPRDPVPPDVTGLYVF
DNA44804 61 EN-----GITMLDAS-----SF
** * . ** *
P_AAB38323 61 ENGITMLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETF
DNA44804 73 AGLPGLQLLDLSQNQIAS-----LRLPRLLLLDLSHNS
** * . * * *
P_AAB38323 121 RGLRRLERLYLGKNRIRHIQPGAFDTLDRLLELKLQDNELRALPPLRLPRLLLLDLSHNS
DNA44804 106 LLALEPGILDTANVEALRLAGLGLQQLDEGLFSRLRNLDLDVSDNQLERVPPVIRGLRG

P_AAB38323 181 LLALEPGILDTANVEALRLAGLGLQQLDEGLFSRLRNLDLDVSDNQLERVPPVIRGLRG
DNA44804 166 LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNSLSLQALPGDLSGLFPRLRLAAARNPF

P_AAB38323 241 LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNSLSLQALPGDLSGLFPRLRLAAARNPF
DNA44804 226 NCVCPLSWFGPWVRESHVTLASPEETRCHFPKPNAGRLLELDYADFGPCATTTTATVPT

P_AAB38323 301 NCVCPLSWFGPWVRESHVTLASPEETRCHFPKPNAGRLLELDYADFGPCATTTTATVPT
DNA44804 286 TRPVVREPTALSSSLAPTWSPTAPATEAPSPSTAPPTVGPVPQDCPPSTCLNGGTC

P_AAB38323 361 TRPVVREPTALSSSLAPTWSPTAPATEAPSPSTAPPTVGPVPQDCPPSTCLNGGTC
DNA44804 346 HLGTRHHLACLCPEGFTGLYCESQMGQTRPSPTPVTPRPPRSLTGIEPVSPTSRLRVGL

P_AAB38323 421 HLGTRHHLACLCPEGFTGLYCESQMGQTRPSPTPVTPRPPRSLTGIEPVSPTSRLRVGL
DNA44804 406 QRYLQGSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCMPLGP

P_AAB38323 481 QRYLQGSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCMPLGP
DNA44804 466 GRVPEGEEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAGVGAAYCVR

P_AAB38323 541 GRVPEGEEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAGVGAAYCVR
DNA44804 526 RGRAMAAAAQDKGVGPGAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFGP

P_AAB38323 601 RGRAMAAAAQDKGVGPGAGPLELEGVKVPLEPGPKATEAVERPCPAGLSVKCHSWASKA
DNA44804 586 PGLQSPLHAKPYI

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P_AAB38323 661 -WPQSPLHAKPYI

>11 P_AAY66643 Membrane-bound protein PRO1282 - Homo sapiens. (611 aa) [1 seg]
Score = 2405 (931 bits); Expect = 0.0
Identities = 502/673 (74%), Positives = 512/673 (75%), Gaps = 137/673 (20%), at
1,1-598,611

DNA44804 1 MCSRVPLLLPLLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF
*****
P_AAY66643 1 MCSRVPLLLPLLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGTTVPRDVPPDTVGLYVF

DNA44804 61 EN-----GITMLDAS-----SF
** * . * *
P_AAY66643 61 ENGITMLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETF
*****

DNA44804 73 AGLPGLQLLDLSQNQIAS-----LRLPRLLLLDLSDHNS
** * . * *
P_AAY66643 121 RGLRRLERLYLGKNRIRHIQPGAFDTLDRLLELKLQDNELRALPPLRLPRLLLLDLSDHNS
*****

DNA44804 106 LLALEPGILDTANVEALRLAGLGLQQLDEGLFSRLRNLDLDVSDNQLERVPPVIRGLRG
*****
P_AAY66643 181 LLALEPGILDTANVEALRLAGLGLQQLDEGLFSRLRNLDLDVSDNQLERVPPVIRGLRG
*****

DNA44804 166 LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNSLSLQALPGDLSGLFPRLRLAAARNPF
*****
P_AAY66643 241 LTRLRLAGNTRIAQLRPEDLAGLAALQELDVSNSLSLQALPGDLSGLFPRLRLAAARNPF
*****

DNA44804 226 NCVCPLSWFGPWVRESHVTLASPEETRCHFPKNAGRLLLELDYADFGCPATTTTATVPT
*****
P_AAY66643 301 NCVCPLSWFGPWVRESHVTLASPEETRCHFPKNAGRLLLELDYADFGCPATTTTATVPT
*****

DNA44804 286 TRPVVREPTALSSSLAPTWSPTAPATEAPSPPSTAPPTVGPVPQPDQCPPSTCLNGGTC
*****
P_AAY66643 361 TRPVVREPTALSSSLAPTWSPTAPATEAPSPPSTAPPTVGPVPQPDQCPPSTCLNGGTC
*****

DNA44804 346 HLGTRHHLACLCPEGFTGLYCESQMGQTRPSPTPVTPRPPRSLTLGIEPVSPTSIRVGL
*****
P_AAY66643 421 HLGTRHHLACLCPEGFTGLYCESQMGQTRPSPTPVTPRPPRSLTLGIEPVSPTSIRVGL
*****

DNA44804 406 QRYLQGSSVQLRSLRLTYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCMPLGP
*****
P_AAY66643 481 QRYLQGSSVQLRSLRLVHSN-----HAPVTQAR-----
*****

DNA44804 466 GRVPEGEEACGEAHTPPAVHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAGVGAAYCVR
* . * * *
P_AAY66643 509 -----EGNLPLLI----APA-----LAAVLLAAL-----AAVGAAYCVR
*****

DNA44804 526 RGRAMAAAAQDKGQVGPAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFGP
*****
P_AAY66643 539 RGRAMAAAAQDKGQVGPAGPLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFGP
*****

DNA44804 586 PGLQSPLHAKPYI
*****
P_AAY66643 599 PGLQSPLHAKPYI

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